

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:09:40 ; Search time: 48 Seconds
 (without alignments)
 23.148 Million cell updates/sec

Title: US-09-772-819-18
 Perfect score: 41
 Sequence: 1 RYVAAHFF 7

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database :

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 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: *
 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 12 41 100.0 7 20 AAY15319
 13 41 100.0 7 21 AAB27418
 14 41 100.0 7 21 AAB28116
 15 41 100.0 7 21 AAY8140
 16 41 100.0 7 21 AAY77053
 17 41 100.0 7 21 AAY7415
 18 41 100.0 7 21 AAE0886
 19 41 100.0 7 22 AAE01003
 20 41 100.0 7 22 AAE03166
 21 41 100.0 7 23 AAE19202
 22 41 100.0 7 23 AAB8782
 23 41 100.0 7 24 ABU1429
 24 41 100.0 7 24 AAE0886
 25 37 90.2 7 19 AAW65609
 26 37 90.2 7 19 AAW4743
 27 37 90.2 7 19 AAW64740
 28 37 90.2 7 19 AAW65634
 29 37 90.2 7 19 AAW65613
 30 37 90.2 7 19 AAW7126
 31 37 90.2 7 19 AAW1122
 32 37 90.2 7 20 AAY19597
 33 37 90.2 7 20 AAY9599
 34 37 90.2 7 20 AAY33912
 35 37 90.2 7 20 AAY12352
 36 37 90.2 7 20 AAY30551
 37 37 90.2 7 20 AAY30553
 38 37 90.2 7 20 AAY30576
 39 37 90.2 7 20 AAY30595
 40 37 90.2 7 20 AAY30597
 41 37 90.2 7 20 AAY32726
 42 37 90.2 7 20 AAY32728
 43 37 90.2 7 20 AAY33780
 44 37 90.2 7 20 AAY33782
 45 37 90.2 7 20 AAY15356

ALIGNMENTS

RESULT 1
 AAW65614

AAW65614 standard; peptide: 7 AA.

XX
 ID AAW65614
 XX
 AC AAW65614;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Angiotensin II analogue.
 XX
 KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor; wound healing.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W09826795-A1.
 XX
 PD 25-JUN-1998.
 XX
 PF 16-DEC-1997; 97K0-US23461.
 XX
 PR 15-DEC-1997; 97US-099064.
 PR 16-DEC-1996; 96US-0028310.
 XX
 PA (UYS-C) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Dizerega GS, Rodgers KE;
 XX
 DR WPI; 1998-362518/31.
 XX
 PT Promoting incorporation of skin graft onto underlying tissue -

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	41	100.0	7	19	AAW65614		Angiotensin II ana
2	41	100.0	7	19	AAW64744		Angiotensin II pe
3	41	100.0	7	20	AAW71270		Peptide used to ac
4	41	100.0	7	20	AAY43600		Angiotensin analog
5	41	100.0	7	20	AAY42353		Angiotensin II ana
6	41	100.0	7	20	AAY30554		Amino acid sequenc
7	41	100.0	7	20	AAY30598		Angiotensin II ana
8	41	100.0	7	20	AAY32749		Angiotensin II ana
9	41	100.0	7	20	AAY32729		Angiotensin II ana

PT Comprises Pre-treating graft with angiotensin II, or analogue or peptide fragment

XX Disclosure; Page 7; 82DP; English.

PS The invention relates to the use of angiotensin II (AII). AII analogues, AII fragments and AII fragment analogues for promoting incorporation of a skin graft into underlying tissue of a mammal. The peptides are effective in accelerating the growth or healing of skin grafts and in accelerating re-epithelialisation and tissue repair, even at very low concentrations. They can significantly accelerate the rate of healing at nanomolar levels in vivo. AII accelerates wound repair by increased reovascularisation, growth factor release, re-epithelialisation, extracellular matrix production, and increased flow of blood and nutrients to the injured tissue. Use of the above peptides other than AII itself, an extremely potent vasoconstrictor, may avoid the side effects of AII, such as increase in blood pressure and thirst. The present sequence represents an angiotensin II analogue.

XX Sequence 7 AA;

Query Match Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVYAHPF 7
Db 1 RVYAHPF 7

RESULT 2
AAW64744
ID AAW64744 Standard; peptide; 7 AA.

XX AAW64744;

XX DT 02-NOV-1998 (first entry)

XX DE Angiotensin III peptide #2.

XX KW Proliferation; mesenchymal stem cell; lineage-specific cell;

XX KW haematopoietic; cell culture; transplantation; treatment; malignant;

XX KW inherited disease; angiotensinogen; angiotensin I; angiotensin III.

XX OS Synthetic.

XX Homo sapiens.

XX PN WO9832457-A2.

XX PD 30-JUL-1998.

XX PF 26-JAN-1998; 98WO-US01552.

XX PR 23-JAN-1998; 98US-01066593.

XX PR 08-MAY-1997; 97US-01036107.

XX PR 28-OCT-1997; 97US-01046859.

XX PR 31-OCT-1997; 97US-01063210.

XX PR 18-NOV-1997; 97US-01065612.

XX PR 26-NOV-1997; 97US-01066593.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI diZerega G, Rodgers KE;

XX DR 1998-437044/37.

XX PT Methods for accelerating thermal wound healing in humans - using

XX PT angiotensinogen II and AII analogues

XX XX

Claim 9; Page 10; 58pp; English.

XX AAW7110-27 represent peptide used in the method of the invention. The

XX specification describes a method of accelerating thermal wound healing

XX in humans. The method comprises applying to the thermally injured tissue

XX an amount of at least one active agent which comprises the peptides

PT Comprises Pre-treating graft with angiotensin II, or analogue or peptide fragment

XX Disclosure; Page 7; 82DP; English.

PS The invention relates to the use of angiotensin II (AII). AII analogues, AII fragments and AII fragment analogues for promoting incorporation of a skin graft into underlying tissue of a mammal. The peptides are effective in accelerating the growth or healing of skin grafts and in accelerating re-epithelialisation and tissue repair, even at very low concentrations. They can significantly accelerate the rate of healing at nanomolar levels in vivo. AII accelerates wound repair by increased reovascularisation, growth factor release, re-epithelialisation, extracellular matrix production, and increased flow of blood and nutrients to the injured tissue. Use of the above peptides other than AII itself, an extremely potent vasoconstrictor, may avoid the side effects of AII, such as increase in blood pressure and thirst. The present sequence represents an angiotensin II analogue.

XX Sequence 7 AA;

Query Match Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 7 AA;

Query Match Score 41; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
AAW71127
ID AAW71127 standard; peptide; 7 AA.

XX AC AAW71127;

XX DT 27-OCT-1998 (first entry)

XX DE Peptide used to accelerate thermal wound healing.

XX AC AAW71127;

XX XX

Angiotensin: AII; acceleration; thermal wound healing; human; growth factor release; neovascularisation; re-epithelialisation; extracellular matrix production.

XX OS Synthetic.

XX PN WO9833813-A2.

XX PD 06-AUG-1998.

XX PR 04-FEB-1998; 98WO-US02049.

XX PR 04-FEB-1997; 97US-0037166.

XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PI diZerega G, Rodgers KE;

XX DR 1998-437391/37.

XX PT Methods for accelerating thermal wound healing in humans - using

XX PT angiotensinogen II and AII analogues

XX XX

Claim 9; Page 10; 58pp; English.

XX AAW7110-27 represent peptide used in the method of the invention. The

XX specification describes a method of accelerating thermal wound healing

XX in humans. The method comprises applying to the thermally injured tissue

XX an amount of at least one active agent which comprises the peptides

CC AAW7115-27: The method can be used to promote the healing of thermal
 CC wounds by accelerating growth factor release, neovascularisation,
 CC re-epithelialisation and extracellular matrix production. The sequences
 CC are analogues of the angiotensin or angiotensinogen family of proteins.
 XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 RYVYAHPF 7
 Db 1 RYVYAHPF 7

RESULT 4

AYA49600
 ID AY49600 standard; peptide, 7 AA.
 XX
 AY49600;
 XX
 13-JAN-2000 (first entry)

DE Angiotensin analogue peptide SEQ ID NO:18.
 KW Angiotensin I; angiotensin II; angiotensinogen; AI; AII; infection;
 KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.
 XX
 Synthetic.
 XX
 WO9952540-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 07-APR-1999; 99WO-US07654.
 XX
 PR 09-APR-1998; 98US-0081262.
 PR 12-JUN-1998; 98US-0089024.
 XX
 PA (WYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Rodgers KE, Dizerega G;

A

XX
 DR; 1999-620285/53.
 XX
 Treating or preventing infections in mammals using peptides derived
 PR from angiotensin or angiotensin receptor agonists.
 XX
 PI Rodgers KE, Dizerega G;

PS Page 12; 91pp; English.

XX
 The present invention describes a method for treating or preventing
 CC infections in mammals by administering peptides (A) that are fragments
 CC or analogues (or their fragments) of angiotensinogen, angiotensins I or
 CC II, or angiotensin II AT 2-type receptor agonists. (A) contain at least
 CC 3 consecutive amino acids (aa) from the R1 and R2 together = X-Ra-Rb-;
 CC R1-R2-R4-R5-R6-R7-R8 (S1); where R1 and R2 together = X-Ra-Rb-;
 CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminoacyl)pentane
 CC carboxylic acid, Ala, dimethylglycine, Pro, betaine, Glu(NH₂), Gly,
 CC Asp(NH₂) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,
 CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,
 CC Ile, Gly, Pro, Alb (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr
 CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or aza-Tyr;
 CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;
 CC R7 = Pro or Ala; R8 = phe, 4-bromo-phe, Ile or Tyr; proviso =
 CC sequences having R4 as a terminal Tyr residue are excluded. The method
 CC is particularly used in cases of bacterial infection (e.g. septic shock,
 CC peritonitis, bacteraemia or endotoxaemia) but also against viral and
 CC parasitic infections. AAY49600 to AAY49623 represent specifically
 CC claimed examples of (A).
 XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 RYVYAHPF 7
 Db 1 RYVYAHPF 7

RESULT 5

f

AYA42353
 ID AY42353 standard; peptide, 7 AA.
 XX
 AY42353;
 XX
 29-NOV-1999 (first entry)

XX
 DE Angiotensin II analogue 22.
 KW embryonic stem cell; ES; angiotensin; totipotent cell;
 KW gene therapy; replacement therapy; angiotensin II; AII;
 KW analogue.

XX
 Homo sapiens.

XX
 WC9942122-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 16-FEB-1999; 99WO-US03243.
 XX
 PR 19-FEB-1998; 98US-0075179.
 XX
 (WYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Dizerega G, Rodgers KE;
 XX
 DR WPI; 1999-527419/44.
 XX
 PT Promoting embryonal cell proliferation, using angiotensinogen and
 PT angiotensin peptides, analogs or fragments
 XX
 PS Claim 2; Page 10; 76pp; English.

XX
 This is the amino acid sequence of the Angiotensin II analogue, 22.
 CC The formation of Angiotensin II (AII) is initiated by the action of
 CC renin on the plasma substrate angiotensinogen.
 CC This results in Angiotensin I (AI) which then converted to AII by the
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu
 residues from AI (AY42352).

CC The active agents, Angiotensinogen, Angiotensin I (AI), AI
 CC analogs, AI fragments and analogs, Angiotensin II (AII), AII analogs,
 CC AII fragments or analogs, or AI/AT 2 receptor agonists can
 CC rapidly provide a large population of ESCs (Embryonic Stem Cell) for use
 CC in replacement therapy. Similarly, methods that increase in vivo
 CC proliferation of ESCs will enhance the utility of replacement therapy by
 CC rapidly increasing local concentration of the stem cells and their
 CC progeny at the site of therapy. The method also increases the potential
 CC utility of ESCs as vehicles for gene therapy in certain disorders by
 CC more efficiently providing a large number of such cells for transfection,
 CC and also by providing a more efficient means to rapidly expand
 CC transfected ESCs.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 RYVYAHPF 7
 Db 1 RYVYAHPF 7

XX WO9939743-A2.
 XX PR 13-NOV-1998; 98US-0108412.
 XX PR 09-FEB-1998; 98US-0074104.
 XX (DIZE/) DIZEREGA G.
 PA (RODG/) RODGERS K. E.
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX PI Dizerega G, Rodgers KE;
 XX DR 1999-508461/42.
 PT Hepatic cell proliferation with angiotensin I and II derived active
 agents, useful for regeneration of liver after resection
 XX PI Dizerega G, Rodgers KE;
 XX PS Claim 2; Page 11; 66pp; English.
 XX DR 1999-508461/42.
 PT Hepatic cell proliferation with angiotensin I and II derived active
 agents, useful for regeneration of liver after resection
 XX PS Claim 2; Page 11; 66pp; English.
 XX Peptides AAY32715-Y32749 are angiotensin II (All) analogues. The
 CC peptides are derived from the All peptide (AY32750). All increases
 CC mitogenesis and chemotaxis in cultured cells, and also increases the
 CC release of growth factors and extracellular matrices. All has also been
 CC shown to increase the proliferation of certain cell types. The All
 CC analogue peptides can be used as the active agent in a method for
 CC promoting hepatic cell proliferation and differentiation. The All
 CC involves contacting the hepatic cells with an amount effective enough to
 CC promote proliferation of any of the peptides. This method is useful in
 CC liver regeneration following resection of hepatocarcinomas, hepatitis
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
 CC failure, hepatocyte transplantation, liver transplantation and other
 CC hepatic disorders where rapid regeneration of the liver is desirable. The
 CC methods are also useful in rapidly providing a large population of
 CC hepatic cells for use in cell therapy and for providing a large
 CC population of transfected hepatic cells for use in gene therapy.
 XX SQ Sequence 7 AA;
 XX Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 RYAHPPF 7
 AC 1 RYAHPPF 7
 DB 1 RYAHPPF 7
 XX RESULT 9
 XX AAY32729
 ID AAY32729 standard; peptide; 7 AA.
 XX DE 09-NOV-1999 (first entry)
 XX AC AAY32729;
 XX DT 09-NOV-1999 (first entry)
 XX DE Angiotensin II analogue 21.
 KW Angiotensin II; All; hepatocyte; proliferation; mitogenesis;
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;
 KW hepatocarcinoma; hepatectomy; transplantation.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9939743-A2.
 XX PD 12-AUG-1999.
 XX PR 08-FEB-1999.
 PF 08-FEB-1999; 99WO-US02618.
 XX PR 13-NOV-1998; 98US-0108412.
 XX PR 09-FEB-1998; 98US-0074104.
 XX (DIZE/) DIZEREGA G.
 PA (RODG/) RODGERS K. E.
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX PI Dizerega G, Rodgers KE;
 XX PS Claim 2; Page 11; 66pp; English.
 XX CC Peptides AAY32715-Y32749 are angiotensin II (All) analogues. The
 CC peptides are derived from the All peptide (AY32750). All increases
 CC mitogenesis and chemotaxis in cultured cells, and also increases the
 CC release of growth factors and extracellular matrices. All has also been
 CC shown to increase the proliferation of certain cell types. The All
 CC analogue peptides can be used as the active agent in a method for
 CC promoting hepatic cell proliferation and differentiation. The All
 CC involves contacting the hepatic cells with an amount effective enough to
 CC promote proliferation of any of the peptides. This method is useful in
 CC liver regeneration following resection of hepatocarcinomas, hepatitis
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic
 CC failure, hepatocyte transplantation, liver transplantation and other
 CC hepatic disorders where rapid regeneration of the liver is desirable. The
 CC methods are also useful in rapidly providing a large population of
 CC hepatic cells for use in cell therapy and for providing a large
 CC population of transfected hepatic cells for use in gene therapy.
 XX SQ Sequence 7 AA;
 XX Query Match 100.0%; Score 41; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 RYAHPPF 7
 AC 1 RYAHPPF 7
 DB 1 RYAHPPF 7
 XX RESULT 10
 XX AAY33783
 ID AAY33783 standard; peptide; 7 AA.
 XX AC AAY33783;
 XX DT 09-NOV-1999 (first entry)
 XX DE Angiotensin II (All) octapeptide analogue 21.
 KW Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;
 KW Parkinson's disease; neuron replacement therapy.
 OS Homo sapiens.
 XX PN WO9942123-A1.
 XX PD 26-AUG-1999.
 XX PR 19-FEB-1999; 99WO-US03772.
 XX PR 19-FEB-1999; 98US-0075232.
 XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 PI Dizerega G, Rodgers KE;
 XX

PF 12-AUG-1999; 99WO-US18374.
 XX
 PR 13-AUG-1998; 98US-0096414.
 PR 18-SEP-1998; 98US-0101024.
 XX
 (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX
 PI Rodgers K, Dizerega G;

XX
 XX
 DR WPI: 2000-237409/20.

XX
 Increasing blood flow to ischemic tissue for minimizing cardiac
 remodelling and development of congestive heart failure involves
 administration of an active agent -

XX
 PS Claim 2: Page 45; 56pp; English.

XX
 The present sequence represents an angiotensin II analogue. The
 specification also describes peptides derived from angiotensinogen,
 angiotensin I, angiotensin II, angiotensin III, and their analogues.
 The peptides are used for increasing blood flow to ischemic tissue.
 The peptides are angiogenesis stimulators. The peptides are useful for
 increasing blood flow to ischemic tissue by stimulating angiogenesis,
 and minimizing cardiac remodelling and development of congestive heart
 disease following a ischemic myocardial infarction. The stimulation of
 angiogenesis is also useful for embryonic development, wound healing
 and treating chronic inflammatory disease.

XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYAHPPF 7
 |||||
 Db 1 RYAHPPF 7

Search completed. November 5, 2003, 18:13:49
 Job time : 49 secs

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3	41	100.0	7	3	US-09-245-680-18	Sequence 18, Appl		
4	41	100.0	7	3	US-09-198-806C-18	Sequence 18, Appl		
5	41	100.0	7	3	US-09-352-191-18	Sequence 18, Appl		
6	41	100.0	7	4	US-09-012-400-18	Sequence 18, Appl		
7	41	100.0	7	4	US-09-264-563-18	Sequence 18, Appl		
8	41	100.0	7	4	US-09-307-940B-18	Sequence 18, Appl		
9	41	100.0	7	4	US-09-657-890-18	Sequence 18, Appl		
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11	41	100.0	7	4	US-09-266-93A-18	Sequence 18, Appl		
12	37	90.2	7	3	US-08-990-664-14	Sequence 18, Appl		
13	37	90.2	7	3	US-08-990-664-18	Sequence 18, Appl		
14	37	90.2	7	3	US-08-990-664-39	Sequence 18, Appl		
15	37	90.2	7	3	US-09-210-249-10	Sequence 18, Appl		
16	37	90.2	7	3	US-09-373-962-13	Sequence 18, Appl		
17	37	90.2	7	3	US-09-373-962-17	Sequence 18, Appl		
18	37	90.2	7	3	US-09-245-80-13	Sequence 18, Appl		
19	37	90.2	7	3	US-09-245-680-17	Sequence 17, Appl		
20	37	90.2	7	3	US-09-198-806C-13	Sequence 13, Appl		
21	37	90.2	7	3	US-09-198-806C-17	Sequence 13, Appl		
22	37	90.2	7	3	US-09-352-191-13	Sequence 13, Appl		
23	37	90.2	7	3	US-09-352-191-17	Sequence 17, Appl		
24	37	90.2	7	4	US-09-012-400-13	Sequence 13, Appl		
25	37	90.2	7	4	US-09-012-400-17	Sequence 17, Appl		
26	37	90.2	7	4	US-09-264-563-13	Sequence 13, Appl		
27	37	90.2	7	4	US-09-264-563-17	Sequence 17, Appl		

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000
 Post-processing: Maximum Match 0%
 Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Total number of hits satisfying chosen parameters: 328717

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:12:56 ; Search time 20 Seconds
 (without alignments)
 14.809 Million cell updates/sec

Title: US-09-772-819-18

Perfect score: 41

Sequence: 1 RYVYAHPP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

ALIGNMENTS

RESULT 1
 US-08-990-664-19
 Sequence 19, Application US/08990664
 Patent No. 6110855
 GENERAL INFORMATION:
 APPLICANT: Rodgers, Kathleen
 TITLE OF INVENTION: METHOD OF PROMOTING HEALING
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESS: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PastSO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/990,664
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/028,310
 FILING DATE: 16-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: USC012.001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 714-760-0404
 TELEFAX: 714-760-9502
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLELC TYPE: peptide
 US-08-990-664-19

Query Match Length DB ID Description

Score 41; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Query 1 RVYAHPF 7
Db 1 RVYAHPF 7

US-09-373-962-18
; Sequence 18, Application US/09373962
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
; FILE REFERENCE: 98364A
; CURRENT APPLICATION NUMBER: US/09/373,962
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AI1 analogue

Query Match 100.0%; Score 41; DB 3; Length 7;
Best Local Similarity 100.0%; Prd. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPF 7
Db 1 RVYAHPF 7

RESULT 5

US-09-352-191-18

Query Match 100.0%; Score 41; DB 3; Length 7;
Best Local Similarity 100.0%; Prd. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPF 7
Db 1 RVYAHPF 7

RESULT 6

US-09-352-191-18

Query Match 100.0%; Score 41; DB 3; Length 7;
Best Local Similarity 100.0%; Prd. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPF 7
Db 1 RVYAHPF 7

RESULT 4

US-09-198-806C-18
; Sequence 18, Application US/09198806C
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem

OTHER INFORMATION: Description of Artificial Sequence:All analogue
JS-09-012-400-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Fred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYUAHPF 7
Db 1 RYUAHPF 7

RESULT 7
US-09-264-563-18
Sequence 18, Application US/09264563A
Patent No. 6455500
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: diZerega, Gere
TITLE OF INVENTION: Radiation Therapy Methods
FILE REFERENCE: 97012K1
CURRENT APPLICATION NUMBER: US/09/264,563A
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-264-563-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Fred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYUAHPF 7
Db 1 RYUAHPF 7

RESULT 8
US-09-307-940B-18
Sequence 18, Application US/09307940B
Patent No. 6415988
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: diZerega, Gere
TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After
TITLE OF INVENTION: Chemotherapy
FILE REFERENCE: 97017P1
CURRENT APPLICATION NUMBER: US/09/307,940B
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-307-940B-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Fred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYUAHPF 7
Db 1 RYUAHPF 7

RESULT 9
US-09-657-890-18
Sequence 18, Application US/09657890
Patent No. 6482800
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: diZerega, Gere
TITLE OF INVENTION: Methods to Stimulate Angiogenesis
FILE REFERENCE: 98367AI
CURRENT APPLICATION NUMBER: US/09/657,890
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-657-890-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Fred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYUAHPF 7
Db 1 RYUAHPF 7

RESULT 10
US-09-266-293A-18
Sequence 18, Application US/09266293A
Patent No. 6498138
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: diZerega, Gere
TITLE OF INVENTION: Method of Promoting Production of Living Tissue
FILE REFERENCE: 98049b
CURRENT APPLICATION NUMBER: US/09/266,293A
CURRENT FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:All analogue
US-09-266-293A-18

Query Match 100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Fred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYUAHPF 7
Db 1 RYUAHPF 7

RESULT 11
US-09-716-394-18
Sequence 18, Application US/09716394
Patent No. 656335
GENERAL INFORMATION:
APPLICANT: University of Southern California
APPLICANT: Rodgers, Kathleen
APPLICANT: diZerega, Gere
TITLE OF INVENTION: Methods for Mobilizing Hematopoietic Progenitor Cells from Bone
TITLE OF INVENTION: into Peripheral Blood in a Patient in Need of Chemotherapy
FILE REFERENCE: 97-017-P8
CURRENT APPLICATION NUMBER: US/09/716,394

CURRENT FILING DATE: 2000-11-20
; PRIORITY APPLICATION NUMBER: US 60/064,908
; PRIORITY FILING DATE: 1998-05-11
; PRIORITY APPLICATION NUMBER: US 60/092,633
; PRIORITY FILING DATE: 1998-07-13
; PRIORITY APPLICATION NUMBER: US 09/307,940
; PRIORITY FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Ala4 All1
; US-09-716-394-18

Query Match 100.0%; Score 41; DB 4; Length 7;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVYAHPPF 7
Dc 1 RVYAHPPF 7

RESULT 13
US-08-990-664-18
; Sequence 18, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; ADDRESS: dizeresa, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; NUMBER OF SEQUENCES: 46
; NUMBER OF SEQUENCES: 46
; TITLE OF INVENTION: IN SKIN GRAFTS
; CURRENT APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION/DOCKET NUMBER: 34.115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-990-664-18

Query Match 90.2%; Score 37; DB 3; Length 7;
; Best Local Similarity 85.7%; Pred. No. 2.5e+05;
; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVYAHPPF 7
Dc 1 RVYGHPPF 7

RESULT 14
US-08-990-664-39
; Sequence 39, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen

INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Other
; LOCATION: 4...4

APPLICANT: dizerega, Gere
 TITLE OF INVENTION: METHOD OF PROMOTING HEALING
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/990,664
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/028,310
 FILING DATE: 16-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Alman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: USCO12.001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 714-760-0404
 TELEFAX: 714-760-9502
 TELEX:
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-990-664-39

Query Match: 90.2%; Score 37; DB 3; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2.5e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0;
 Gaps 0;
 Qy 1 RVVYHPPF 7
 Db 1 RVVYHPPF 7

RESULT 15
 US-09-210-249-10
 Sequence 10, Application US/09210249A
 Patent No. 6165578
 GENERAL INFORMATION:
 APPLICANT: dizerega, Gere
 TITLE OF INVENTION: WOUND HEALING COMPOSITIONS
 FILE REFERENCE: USC013.001A
 CURRENT APPLICATION NUMBER: US/09/210,249A
 CURRENT FILING DATE: 1998-12-11
 EARLIER APPLICATION NUMBER: 60/069,662
 EARLIER FILING DATE: 1997-12-12
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 10
 LENGTH: 7
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic peptide
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (4) . . . (4)

TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
TITLE OF INVENTION: Differentiation
FILE REFERENCE: 97,017,FLA
CURRENT APPLICATION NUMBER: US/09/837,697A
CURRENT FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 37
SEQ ID NO: 18
SOFTWARE: PatentIn version 3.1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: All analogue
US-09-837-697A-18

RESULT 3
US-09-900-936-18
Sequence 18, Application US/09900936
PATENT NO. US20020165141A1
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: dizeresa, Gere
TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
FILE REFERENCE: 00-506-A
CURRENT APPLICATION NUMBER: US/09/900,936
CURRENT FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:AI: analogue
US-09-900-936-18

Query Match Score 41; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 RYTAHPPF 7
Db 1 RYTAHPPF 7

Query Match Score 41; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 RYTAHPPF 7
Db 1 RYTAHPPF 7

RESULT 4
US-09-772-819-18
Sequence 18, Application US/09772819
Publication No. US20030199434A1
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
APPLICANT: dizeresa, Gere
TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
FILE REFERENCE: 98165B
CURRENT APPLICATION NUMBER: US/09/772,819
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 18
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:AI1 analogue
US-09-772-18

Query Match 100.0%; Score 41; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYVYAHFF 7
      ||||| |
Db 1 RYVYAHFF 7

RESULT 5
JS-10-341-001-18
; Sequence 18, Application US/10341001
; Publication No. US20030130196A1
; GENERAL INFORMATION:
;   APPLICANT: Rodgers, Kathleen
;   TITLE OF INVENTION: Radiation Therapy Methods
;   FILE REFERENCE: 9701TKS
;   CURRENT APPLICATION NUMBER: US/10/341,001
;   CURRENT FILING DATE: 2003-01-13
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 18
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AI1 analogue
US-10-341-001-18

Query Match 100.0%; Score 41; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYVYAHFF 7
      ||||| |
Db 2 RYVYAHFF 7

RESULT 6
US-39-771-192-13
; Sequence 13, Application US/09771192
; Patent No. US2002049162A1
; GENERAL INFORMATION:
;   APPLICANT: Rodgers, Kathleen
;   TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
;   FILE REFERENCE: 99-1043-A
;   CURRENT APPLICATION NUMBER: US/09/771,192
;   CURRENT FILING DATE: 2001-01-26
;   NUMBER OF SEQ ID NOS: 51
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 13
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:AI1 analogue
;   NAME/KEY: MOD_RES
;   LOCATION: (4)
;   OTHER INFORMATION: Nle
US-09-771-192-13

Query Match 90.2%; Score 37; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RYVYAHFF 7
      ||||| |

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Db 1 RVYXHPF 7

RESULT 7
 US-09-771-192-17
 ; Sequence 17, Application US/09771192
 ; Patent No. US20020049162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen E.
 ; FILE REFERENCE: 99-1043-A
 ; CURRENT APPLICATION NUMBER: US/09/771.192
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 17
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:AI1 analogue
 ; US-09-771-192-17

Query Match 90.2%; Score 37; DB 9; Length 7;
 Best Local Similarity 85.7%; Pred. No. 5.8e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 8
 US-09-837-697A-13
 ; Sequence 13, Application US/09837697A
 ; Patent No. US20020146823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; FILE REFERENCE: 97-017-F1A
 ; CURRENT FILING DATE: 2002-02-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 13
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: AI1 analogue
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (4) .. (4)
 ; OTHER INFORMATION: Nle
 ; US-09-837-697A-13

Query Match 90.2%; Score 37; DB 10; Length 7;
 Best Local Similarity 85.7%; Pred. No. 5.8e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 9
 US-09-837-697A-17
 ; Sequence 17, Application US/09837697A
 ; Patent No. US20020146823A1
 ; GENERAL INFORMATION:

NUMBER OF SEQ ID NCS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
; US-09-930-936-17

Query Match 90.2%; Score 37; DB 12; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
US-09-772-819-13
; Sequence 13, Application US/0977288.9
; Publication No US2003C139434A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; FILE REFERENCE: 98365b
; CURRENT APPLICATION NUMBER: US/09772,819
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: Nle
; US-09-772-819-13

Query Match 90.2%; Score 37; DB 12; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
US-10-341-001-17
; Sequence 17, Application US/10341001
; Publication No. US20030130196A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K5
; CURRENT APPLICATION NUMBER: US/10/341,901
; CURRENT FILING DATE: 2003-01-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue
; US-10-341-001-17

Query Match 90.2%; Score 37; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYAHPP 7
Db 1 RYXHPP 7

RESULT 13
US-09-772-819-17
; Sequence 11, Application US/09772819
; Publication No. US2003013943A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
; FILE REFERENCE: 98365b
; CURRENT APPLICATION NUMBER: US/09772,819
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

Dp 1 RVYGHPE 7

Search completed: November 5, 2003, 18:21:06
Job time : 41 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 5, 2003, 18:11:10 ; Search time 25 Seconds
(without alignments),
26.927 Million cell updates/sec

Title: US-09-772-819-18
Perfect score: 41
Sequence: 1 RYVYAHPF 7

Scoring table: BLOSUM62
GapP 1c.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR76:*

1: Dir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	37	90.2	10	2	A6J624		angiotensin I - Ga
2	37	90.2	10	2	A90917		angiotensin precursor
3	36	89.2	10	2	A90345		angiotensin I - ho
4	36	87.8	10	2	S65432		Crinia-angiotensin
5	36	87.8	11	2	S07207		angiotensin precursor
6	36	87.8	14	2	A01250		angiotensin I precursor
7	36	87.8	15	2	A60834		angiotensin I precursor
8	36	87.8	476	1	JC2318		angiotensin precursor
9	36	87.8	477	1	ANR		angiotensin precursor
10	36	87.8	477	1	A29978		angiotensin precursor
11	36	87.8	485	1	ANHU		angiotensin precursor
12	35	85.4	146	2	AEC982		probable acetyltransferase
13	35	85.4	329	2	S283C5		hypothetical protein
14	35	87.4	743	2	B88551		ribosomal protein
15	34	82.9	374	2	B82572		P-protein XPF2325
16	33	80.5	424	2	S62190		glycine hydroxymethyltransferase
17	33	80.5	444	2	B64119		Glucose-1-phosphatase
18	33	80.5	751	2	T02858		hypothetical protein
19	32	78.0	83	1	C42645		ribosomal protein
20	32	78.0	83	2	F81664		probable NAD(P)H oxidase
21	32	78.0	176	1	F64725		probable NAD(P)H oxidase
22	32	78.0	176	2	AB5486		probable NAD(P)H oxidase
23	32	78.0	176	2	A90635		probable NAD(P)H oxidase
24	32	78.0	176	2	A10512		probable NAD(P)H oxidase
25	32	78.0	211	2	B70563		probable NAD(P)H oxidase
26	32	78.0	232	2	JC4755		probable NAD(P)H oxidase
27	32	78.0	324	2	E84918		probable NAD(P)H oxidase
28	32	78.0	346	2	S73760		probable NAD(P)H oxidase
29	32	78.0	388	1	S52149		probable NAD(P)H oxidase

RESULT 3

30	32	78.0	424	2	C70651	hypothetical protein
31	32	78.0	428	2	F6050	glycine hydroxymethyltransferase
32	32	78.0	431	1	C91163	glucose-1-phosphatase
33	32	78.0	431	2	DB8009	glucose-1-phosphatase
34	32	78.0	431	2	AH095	hypothetical protein
35	32	78.0	482	2	S23532	methionyl-tRNA synthetase
36	32	78.0	516	2	AH7760	hypothetical protein
37	32	78.0	516	2	F97541	methionyl-tRNA synthetase
38	32	78.0	601	2	T21814	hypothetical protein
39	32	78.0	713	2	T21201	hypothetical protein
40	32	78.0	845	2	H71317	probable methyl-accepting sugar-binding protein
41	32	78.0	1436	2	A99115	hypothetical protein
42	32	78.0	128	2	GB1220	hypothetical protein
43	31	75.6	132	2	FB800	hypothetical protein
44	31	75.6	205	2	G75535	deoxyguanosine kinase

ALIGNMENTS

RESULT 1							
A60624							
angiotensin I - Japanese quail							
C;Species: Coccinrix coccinix japonica (Japanese quail)							
C;Date: 28-Apr-1993 #Sequence_revision 28-Apr-1993 #text_change 07-May-1999							
C;Accession: A60624							
R;Takei, Y.; Hasagawa, Y.							
Gen. Comp. Endocrinol. 79, 12-22, 1990							
A;Title: Vasopressor and depressor effects of native angiotensins and inhibition of the							
A;Reference number: A60624 ; MUID:90284684 ; PMID:2191893							
A;Accession: A60624							
A;Molecule type: protein							
A;Residues: 1-10 <TAK>							
C;Superfamily: antithrombin III							
C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor							
Query Match	90.2%	Score 37;	DB 2;	Length 10;			
Best Local Similarity	85.7%	Pred. No.	0.15;				
Matches	6;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;	C;
Qy	1 RYVYAHPF 7	Db	2 RYVYAHPF 8				
RESULT 2							
A90917							
angiotensin precursor - chicken (fragment)							
C;Accession: A90917 ; A01250							
R;Nakajima, T.; Sokabe, H.							
Chem. Pharm. Bull. 21, 2085-2087, 1973							
A;Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and 21							
A;Reference number: A90917 ; MUID:74127845 ; PMID:4361802							
A;Accession: A90917							
A;Molecule type: protein							
A;Residues: 1-10 <NAK>							
C;Keywords: blood pressure control; hormone; vasoconstrictor							
F;1-10/Product: angiotensin I #status experimental <AN1>							
F;1-8/Product: angiotensin II #status experimental <AN2>							
Query Match	90.2%	Score 37;	DB 2;	Length 10;			
Best Local Similarity	85.7%	Pred. No.	0.15;				
Matches	6;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;	C;
Qy	1 RYVYAHPF 7	Db	2 RYVYAHPF 8				

RESULT 6

A90345
 angiotensin precursor - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
 C;Accession: A90345; ACI1250_0.
 R;Fernley, R.T.; Peart, W.S.
 Bichem, J. 65, 246-254, 1957
 A;Title: The amino acid sequence in a hypertensin.
 A;Accession: A90345
 A;Molecule type: protein
 A;Residues: 110 <ELL>
 C;Keywords: blood pressure control; hormone; vasoconstrictor
 F;1-10/Product: angiotensin I #status experimental <AN1>
 F;1-8/Product: angiotensin II #status experimental <AN2>
 Query Match Score 37; DB 2; Length 10;
 Best Local Similarity 95.7%; Pred. No. 0.25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RYVAAHPF 7
 Db 2 RYVTHHPF 8

RESULT 4

S65432
 angiotensin I - horn fly (fragment)
 C;Species: Haematobia irritans (horn fly)
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S65432
 R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P.
 Eur. J. Biochem. 237, 414-423, 1996
 A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
 A;Accession: S65432
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <WJ>
 A;Note: the source is designated as Haematobia irritans exigua

Query Match Score 36; DB 2; Length 10;
 Best Local Similarity 85.7%; Pred. No. 0.24;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RYVAAHPF 7
 Db 2 RYVTHHPF 8

RESULT 5

S07207
 Crinia-angiotensin, skin - frog (Crinia georgiana)
 C;Species: Crinia georgiana
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
 C;Accession: S07207
 R;Fraspaner, V.; Neichiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
 A;Title: Amino acid composition and sequence of Crinia-angiotensin, an angiotensin II-like peptide: 1132-1133, 1979
 A;Accession number: S07207; MUID:80C4575; PMID:488254
 A;Molecule type: protein
 A;Residues: 1-11 <ERS>
 C;Superfamily: unassigned animal peptides

Query Match Score 36; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 0.27;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RYVAAHPF 7
 Db 2 RYVTHHPF 11

RESULT 7

A60834
 angiotensin I precursor - dog (fragment)
 N;Alternate names: angiotensinogen I
 N;Contains: angiotensin I
 C;Species: Canis lupus familiaris (dog)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
 C;Accession: A60834
 R;Oliver, J.A.
 Hypertension 11, 21-27, 1988
 A;Title: Purification and partial characterization of canine angiotensinogen.
 A;Reference number: A60834; MUID:88119996; PMID:3338837
 A;Accession: A60834
 A;Molecule type: protein
 A;Residues: 1-15 <OLI>
 C;Superfamily: antithrombin III
 C;Keywords: glycoprotein; Plasma
 F;1-10/Product: angiotensin I #status predicted <MAT>
 Query Match Score 36; DB 2; Length 15;
 Best Local Similarity 85.7%; Pred. No. 0.37;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RYVAAHPF 7
 Db 2 RYVTHHPF 8

RESULT 8

JC2318
 angiotensin precursor - sheep
 C;Species: Ovis orientalis aries (domestic sheep)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C;Accession: JC2318; A24406
 R;Nagase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura, Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
 A;Title: Sequencing and expression of sheep angiotensinogen cDNA.
 A;Reference number: JC2318; MUID:95072318; PMID:7765514
 A;Accession: JC2318
 A;Molecule type: RNA
 A;Residues: 1-476 <NAG>
 A;Cross-references: DDBJ:017520; NID:9575533; PIDN:BA004470.1; PID:91197183
 A;Experimental source: liver
 A;Note: the authors translated the codon TTC for residue 465 as Leu
 R;Fernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.

Eur. J. Biochem. 154, 597-601, 1986
 A;Title: Purification and characterization of ovine angiotensinogen.
 A;Reference number: A25406; MUID:86136039; PMID:3081342
 A;Accession: A25406
 A;Molecule type: protein
 A;Residues: 1-37, 'X', 39 <FER>
 C;Superfamily: antithrombin III
 C;Keywords: blood pressure control; glycoprotein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;24-476/Product: angiotensinogen #status predicted <MP1>
 F;25-34/Product: angiotensin #status predicted <MP1>
 F;295-362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 87.8%; Score 36; DB 1; Length 476;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVYAHPPF 7
 Db 26 RYVYIHPF 32

RESULT 9
 ANPT angiotensin precursor - rat
 N;Contains: angiotensin I; angiotensin II; angiotensin III
 C;Species: *Rattus norvegicus* (Norway rat)
 C;Date: 13-Jun-1983 #sequence revision 13-Jun-1993 #text_change 18-Jun-1999
 C;Accession: A0125;
 R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakaniishi, S.
 PROC. NATL. ACAD. SCI. U.S.A. 80, 2196-2200, 1983
 A;Title: Cloning and sequence analysis of cDNA for rat angiotensinogen.
 A;Reference number: A93945; MUID:83169349; PMID:6572971
 A;Accession: A93945
 A;Molecule type: mRNA
 A;Residues: 1-477 <OHK>
 A;Cross-references: GB:100094; GB:JC0704; NID:9202912; PID:AAH98779.1; PMID:9202914
 R;Bounik, J.; Clauser, E.; Strosberg, D.; Freney, J.P.; Menard, J.; Corvol, P.
 A;Title: Rat angiotensinogen and Des(1'2')angiotensinogen: purification, characterisation and cDNA cloning.
 A;Accession: A90456
 A;Molecule type: protein
 A;Residues: 1-485 <QOU>
 C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted in the lung. Angiotensinogen converts angiotensin I and angiotensin II to angiotensin III by dipeptidyl carboxypeptidase I. Angiotensinogen is synthesized in the liver and secreted into the plasma. The gene for angiotensinogen is located on chromosome 10 at 70,000-70,500.
 C;Superfamily: antithrombin III
 C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-477/Product: angiotensinogen #status predicted <MP1>
 F;25-54/Domain: angiotensin II #status experimental <PP1>
 F;26-122/Product: angiotensin III #status experimental <PP2>
 F;26-319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 87.8%; Score 36; DB 1; Length 477;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVYAHPPF 7
 Db 26 RYVYIHPF 32

RESULT 10
 A29978 angiotensin precursor - mouse
 C;Species: *Mus musculus* (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A29978
 R;Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
 Genomics 2, 240-248, 1988
 A;Title: Molecular cloning of the mouse angiotensinogen gene.
 A;Reference number: A29978; MUID:88284703; PMID:3397061
 A;Accession: A29978
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-477 <CLO>
 A;Cross-references: GB:AF045887; PID:J03046; NID:92842773; PIDN: AAC01765.1; PMID:9284277;
 C;Genetics:
 A;Introns: 277/1; 366/2; 414/3
 C;Superfamily: antithrombin III
 C;Keywords: blood pressure control
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-477/Product: angiotensinogen #status predicted <MP1>
 C;Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match Score 87.8%; Score 36; DB 1; Length 477;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVYAHPPF 7
 Db 26 RYVYIHPF 32

RESULT 11
 ANPT angiotensin precursor [validated] - human
 N;Contains: angiotensinogen
 N;Contains: angiotensin I; angiotensin II; angiotensin III
 C;Species: Homo sapiens (man)
 C;Date: 06-Jul-1982 #sequence revision 19-Jan-1996 #text_change 08-Dec-2000
 C;Accession: A35203; A31362; T31168; T31169; A60825; T39482; A90226; 254281; A1
 R;Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami, J.; Biol. Chem. 265, 7576-7582, 1990
 A;Title: Structure and expression of the human angiotensinogen gene. Identification of A;Reference number: A35203; MUID:90237063; PMID:1692023
 A;Accession: A35203
 A;Molecule type: DNA
 A;Residues: 1-485 <FUK>
 A;Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327
 R;Gailard, I.; Clauser, E.; Corvol, P.
 A;Title: Structure of human angiotensinogen gene.
 A;Reference number: A31362; MUID:89170129; PMID:2924688
 A;Accession: A31362
 A;Molecule type: DNA
 A;Residues: 1-267, 'M', 269-332, 'E', 334-485 <DAI>
 A;Cross-references: GB:M24685; GB:M24687; GB:M24688
 A;Note: the authors translated the codon GAA for residue 333 as Gln
 R;Nibu, Y.; Takahashi, S.; Tada, M.; Fukamizu, A.
 J. Biol. Chem. 269, 28598-28605, 1994
 A;Title: Identification of cell type-dependent enhancer core element located in the 3'-untranslated region.
 A;Accession: I37168; MUID:95050659; PMID:7961807
 A;Accession: I37168
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-285 <NIB2>
 A;Cross-references: EMBL:X15324; NID:928695
 A;Accession: I37169
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 287-375 <NIB2>
 A;Cross-references: EMBL:X15325; NID:928695
 A;Accession: I37169
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Accession: A60825; PMID:87212053; PMID:3579322
 A;Cross-references: A60825
 A;Molecule type: mRNA
 A;Residues: 32-184 <KN11>
 R;Kunapuli, S.P.; Kumar, A.

CIRC. Res. 60, 786-790, 1987
 A;Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of a single gene
 A;Reference number: I39463; MUID:87244745; PMID:2885106
 A;Accession: I39462
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-267 'M', 269-338 <KUN2>
 A;Cross-references: GB:M69110; NCBI:978643; PID:9553181
 A;Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequence
 A;Reference number: A90487; MUID:85030455; PMID:609875
 A;Accession: A90487
 A;Molecule type: mRNA
 A;Residues: 1-267 'M', 269-338 <KAG>
 A;Cross-references: GB:K0215; NCBI:9178639; PID:AA51731.1; PID:9178640
 A;Note: it is uncertain whether Met-1 or Met-10 is the initiator
 R;Tewksbury, D.A.; Dart, R.A.; Travis, J.
 Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981
 A;Title: The amino terminal amino acid sequence of human angiotensinogen.
 A;Reference number: A90226; MUID:8125848; PMID:7259779
 A;Accession: A90226
 A;Molecule type: protein
 A;Residues: 34-46 'X', 48-50, 'S', 52-57, 'D' <TEW>
 R;Hixson, J.E.; Powers, P.K.
 Hum. Genet. 96, 110-112, 1995
 A;Title: Detection and characterization of new mutations in the human angiotensinogen gene
 A;Reference number: I54281; MUID:9531754; PMID:7607642
 A;Accession: I54281
 A;Molecule type: DNA
 A;Residues: 176-241, 'I', 243-267 'M', 269-287, 'ANLSAG', <HIX>
 A;Cross-references: GB:S78329; NCBI:99931; PID:AD14281.1; PID:94261987
 C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted in the lungs
 C;Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and angiotensin II is converted to angiotensin III by dipeptidyl carboxypeptidase I.
 C;Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels, by inducing thirst.
 C;Comment: Angiotensin II and angiotensin III are equally potent in stimulating the sympathetic nervous system.
 C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma. The C;Genetics:
 A;Gene: GDB:ACT
 A;Cross-references: GDB:118750; OMIM:1C6150
 A;Map position: 1C42-1C43
 A;Introns: 286/1; 375/2; 422/3
 C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
 C;Superfamily: antithrombin III
 C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
 F;1-33;Domain: (or 1-33) signal sequence #status predicted <SIG>
 F;34-43;Product: angiotensinogen #status predicted <MPT>
 F;34-43;Product: angiotensinogen #status experimental <PP1>
 F;34-41;Product: angiotensin III #status experimental <PP3>
 F;41-170;328;Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match Score 87.8%; Best Local Similarity 85.7%; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Query 1 RVYAHBF 7
 DB 35 RVYAHBF 41
 RESULT 12
 AE0382 probable acetyltransferase STY4159 [imported] - *Salmonella enterica* subsp. *enterica* sero C;Species: *Salmonella* enterica subsp. *enterica* serovar Typhi
 A;Note: this species has also been called *Salmonella* typhi
 C;Accession: AE0382
 C;Accession: AE0382 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.;
 S.; McEule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skeilton, J.; Stevens, K.
 A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AE0382
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-146 <PAR>
 A;Cross-references: GB:AL513382; PID:CAD07985.1; PID:91650497; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY4159
 C;Superfamily: Escherichia coli hypothetical 16.4K protein (rrfE-metA) intergenic region

Query Match Score 85.4%; Best Local Similarity 85.3%; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Query 2 RVYAHBF 7
 DB 22 RVYAHBF 27
 RESULT 13
 S28305 hypothetical protein T23G5.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 12-May-1993 #sequence_revision 12-Mar-1993 #text_change 30-Sep-1993
 C;Accession: S28305
 R;Beck, M.
 submitted to the EMBL Data Library, December 1992
 A;Reference number: S28306
 A;Accession: S28305
 A;Molecule type: DNA
 A;Residues: 1-329 <BBR>
 A;Cross-references: EMBL:Z19158
 C;Genetics:
 A;Introns: 21/3; 115/3; 193/1; 235/i; 259/i
 Query Match Score 85.4%; Best Local Similarity 71.4%; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Query 1 RVYAHBF 7
 DB 10 RVYAHBF 16
 RESULT 14
 S88551 protein T23G5.2 [imported] - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Accession: 10-May-2001 #sequence_revision 10-May-2001
 C;Accession: B88551
 R;Anonymous: The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A;Reference number: A75000; MUID:9906913; PMID:9851916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A;Accession: B88551
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-743 <STO>
 A;Cross-references: GB:chr_III; PID:CAA79573.1; PID:93880120; GSPDB:GN00021; CESP:T23G
 A;Map position: 3
 C;Genetics:
 A;Gene: T23G5.2
 Query Match Score 85.4%; Best Local Similarity 71.4%; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RYVAAHPF 7
 Db 10 RYVAAHPF 16

RESULT 15

B82572 Protein Xf2325 [imported] - *Xylella fastidiosa* (strain: 9a5c)
 C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Feb-2003
 C:Accession: B82572
 C:Name: The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A8515; MUID:20365117; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: B82572
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-374 <SIM>
 A:Cross-references: GB:AE004043; GB:AE003649; NID:9107466; PIDN:AF85124.1; GSDB:GN001
 A:Experimental source: strain 9a5c
 R:ISimpson, A.J.G.; Reinach, F.C.; Arreda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froeh
 J.D.; Jurqueira, M.L.; Kempfer, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laing
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 F.G.; Nunes, L.R.; Oliveira, M.A.; Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.
 A:Authors: Ross, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
 M.; Tsuhako, M.H.; Valada, H.; Van Siuys, M.A.; Vez-Jovski-Aimeida, S.; Vettore, A.L.; 2
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2325

C:Superfamily: bifunctional chorismate/prephenate dehydratase (P-protein); prephe

Query Match 82.9% Score 34; DB 2; Length 374;
 Best Local Similarity 83.3%; Pred: No. 31;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RYVAAHP 6
 Db 201 RYVAAHP 206

Search completed: November 5, 2003, 18:15:29
 Job time : 27 secs

Scoring table:	BLOSUM62						
Scorers:	Gapep 10.0 , Gapext 0.5						
Total number of hits satisfying chosen parameters:	127863						
Minimum DB seq length: 0							
Maximum DB seq length: 2000000000							
Post-processing: Minimum Match 0%							
Post-processing: Maximum Match 100%							
Database : SwissProt_41.1*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	127863						
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	Description
1	3.7	90.2	10	1	ANGI_BOVINA	Q10591	bothrops ja
2	3.7	90.2	10	1	ANGT_BOVINA	P01017	bos taurus
3	3.7	90.2	10	1	ANGT_CHICK	P01018	gallus gallus
4	3.6	87.8	8	1	ANG2_BOTHPSA	Q10592	bothrops ja
5	3.6	87.8	11	1	ANGT_CRIGE	P09037	crinia georgica
6	3.6	87.8	14	1	ANGT_HORSE	P01016	equus caballus
7	3.6	87.8	476	1	ANGT_SHEEP	P20757	ovis aries
8	3.6	87.8	477	1	ANGT_MOUSE	P11859	mus musculus
9	3.6	87.8	477	1	ANGT RAT	P01015	rattus norvegicus
10	3.6	87.8	477	1	ANGT_HUMAN	P01013	homo sapiens
11	3.5	85.4	743	1	YNC2_CABEL	Q03606	caenorhabditis elegans
12	3.4	82.9	544	1	H15_DROME	Q94890	drosophila melanogaster
13	3.3	80.5	424	1	GLY2_HABIN	P50436	haemophilus suis
14	3.3	80.5	437	1	GLGC_PASMU	P43736	haemophilus suis
15	3.3	80.5	439	1	GLGC_PASMU	Q9C292	pasteurella chlamydiae
16	3.2	78.0	83	1	RS17_CHLMLU	P28545	chlamydial
17	3.2	78.0	176	1	YABF_ECOLI	P31577	escherichia coli
18	3.2	78.0	221	1	RL1A_SCPO	Q9P127	schizosaccharomyces pombe
19	3.2	78.0	221	1	RL1B_SCPO	Q9P769	schizosaccharomyces pombe
20	3.2	78.0	346	1	Y285_MYCPN	P75380	mycoplasma pneumoniae
21	3.2	78.0	388	1	AMSL_SRWAM	Q46639	erwinia amylovora
22	3.2	78.0	423	1	GLYA_METH	Q27433	methanobacter
23	3.2	78.0	83	1	RS17_CHLMLU	P00584	escherichia coli
24	3.2	78.0	430	1	GLGC_ECOLI	Q8z233	salmonella enterica
25	3.2	78.0	431	1	GLGC_SALTI	P05415	salmonella enterica
26	3.2	78.0	431	1	GLGC_SALTY	Q8uf52	agrobacteri
27	3.2	78.0	516	1	SYM_FGRTS	Q97hm3	thermoplasm
28	3.2	78.0	1087	1	DP2L_THBAC	Q87q5	methanosa
29	3.2	78.0	1088	1	DP2L_METTAC	Q8px22	methanosa
30	3.2	78.0	1145	1	DP2L_METTMA	Q10519	mycobacterium
31	3.1	75.6	255	1	YM37_MYCTU	Q26293	methanobacter
32	3.1	75.6	304	1	Y1911_METHTH		

ALIGNMENTS							
RESULT 1							
ANGI_BOVINA	ID	ANGI_BOVINA	STANDARD;	PRT;	10 AA.		
Q10591;	AC	Q10591;					
01-OCT-1996 (Rel.	DT	01-OCT-1996 (Rel.	34, Created)				
15-DEC-1998 (Rel.	DT	15-DEC-1998 (Rel.	37, Last sequence update)				
Angiotensin-like Peptide I (Fragment).	DE						
Bothrops jararaca (Jararaca).	OS						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.	OC						
NCBI_TaxID=8724;	RK						
SEQUENCE:	R2	SEQUENCE:					
RC TISSUE=Plasma;	RX	MEDLINE=96208932; PubMed=8829801;					
Borghersi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.; "Isolation and identification of angiotensin-like peptides from the plasma of the snake Bothrops jararaca.", Comp. Biochem. Physiol. 113B:467-473 (1996).	RT						
CC '- SIMILARITY: BELONGS TO THE SERPIN FAMILY.	CC						
InterPro; IPR00215; Serpin.	DR						
PS00284; SERPIN; PARTIAL.	KW						
Vasoconstrictor; Plasma; Serpin.	KW						
NON_TER 10	FT						
SEQUENCE 10 AA: CEF50DD761F2DB42 CRC64;	SQ						
Query Match 90.2%; Best Local Similarity 85.7%; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	1 RYVAYHPF 7					
Db 2 RYVYHPPF 8	Db						
RESULT 2							
ANGT_BOVIN	ID	ANGT_BOVIN	STANDARD;	PRT;	10 AA.		
Q10591;	AC	Q10591;	01, Created)				
21-JUL-1986 (Rel.	DT	21-JUL-1986 (Rel.	01, Last sequence update)				
15-SEP-2003 (Rel.	DT	15-SEP-2003 (Rel.	42, Last annotation update)				
Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin I (Ang II); Angiotensin III (Ang III) (Des-Asp1)-angiotensin II]	DE						
(Fragment).	DE						
AGT OR SERPINA8.	GN						
Bos taurus (Bovine).	OS						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruminantia; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae; Bovidae; Bovinae; Bos.	OC						
NCBI_TaxID=9913;	RK						
SEQUENCE:	RK						
Elliott D.F., Peart W.S.;	RA						

"The amino acid sequence in a hypertensin.";

Biochem. J. 65:246-254(1957).

-!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINogen. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the plasma.

-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

PIR: A90345; A90345.

PDB: 3ERS; 3ERS5; 15-JUL-92.

Inte-Pro; IPR00215; Serpin.

PROSITE: PS00284; SERPIN; PARTIAL.

Vasoconstrictor; Plasma; Serpin; 3D-structure.

PEPTIDE 1 10 ANGIOTENSIN I.

PEPTIDE 1 8 ANGIOTENSIN II.

PEPTIDE 2 8 ANGIOTENSIN III.

NON-TER 10 10

SEQUENCE 10 AA; 1282 MW; CBFBD761F2DB42 CRC64;

Query Match: 90.2%; Score: 37; DB: 1; Length: 10;

Best Local Similarity: 85.7%; P-req. No. 0.11;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps

1 RYAHPPF 7

1 ||| |||

2 RYVHPFP 8

RESULT 3

SEQUENCE: CCGT CHICK STANDARD; PRT; 10 AA.

P01018; 21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)] (Fragment).

AGT OR SERPINs.

Gallus gallus (Chicken), and

Coturnix coturnix japonica (Japanese quail).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauaria; Aves; Neognathae; Galiiformes; Phasianidae; Phasianinae; Gallus.

NCBI_TaxID=9031; 93934;

(1)

SEQUENCE.

SPECIES: Chicken;

MSDLINE: 74127845; PubMed=4361802;

Nakayama T.; Nakajima T.; Sokabe H.; "Comparative studies on angiotensins. 3. Structure of fowl angiotensin and its identification by DNS-method.,"

Gen. Comp. Endocrinol. 79:12-22(1990).

-!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.

RESULT 4 ANGT-TRIGE ID - ANGT CRIGE AC 209057; DT 01-NOV-1988 (Rel. 09, Created) DT 15-SEP-2003 (Rel. 42, Last annotation update) DB Crinia-angiotensin II OS Crinia georgiana (Quacking frog). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachinae; Crinia. RN 8374; SEQUENCE							
Query Match: BELONGS TO THE SERPIN FAMILY.							
DR	A60624; A60624;	PIR; A90917; A90917;	DR	ANGT-TRIGE	STANDARD;	PRT;	8 AA.
DR	InterPro; IPR00215; Serpin.	DR	ANGT CRIGE	STANDARD;	PRT;	8 AA.	
DR	PROSITE; PS0284; SERPIN; PARTIAL.	AC	209057;				
VASSOCONSTRICTOR; PLASMA; Serpin.	PT	ANGT-TRIGE	STANDARD;				
KW	ANGIOTENSIN I.	PT	ANGT CRIGE	STANDARD;			
ANGIOTENSIN II.	PEPTIDE	ANGIOTENSIN III.	PT	ANGT-TRIGE	STANDARD;		
ANGIOTENSIN III.	PEPTIDE	ANGIOTENSIN III.	PEPTIDE	ANGT CRIGE	STANDARD;		
ANGIOTENSIN III.	FT	ANGIOTENSIN III.	FT	ANGT-TRIGE	STANDARD;		
NON-TER	FT	ANGIOTENSIN III.	NON-TER	ANGT CRIGE	STANDARD;		
SEQUENCE	10 AA;	10 AA;	10 AA;	ANGIOTENSIN I.	ANGIOTENSIN I.	ANGIOTENSIN I.	
Query Match: BELONGS TO THE SERPIN FAMILY.	Score: 37;	DB 1;	Score: 37;	DB 1;			
Best Local Similarity: 85.7%;	Pred. No. 0.11;		Best Local Similarity: 85.7%;	Pred. No. 0.11;			
Matches 6; Conservative 0; Mismatches 0;			Matches 6; Conservative 0; Mismatches 0;				
2y	1 RYVYAHFF 7		2y	1 RYVYAHFF 7			
Dy	2 RYVYAHFF 8		Dy	2 RYVYAHFF 8			
RESULT 5 ANGT-TRIGE ID - ANGT CRIGE AC 209057; DT 01-NOV-1988 (Rel. 09, Created) DT 15-SEP-2003 (Rel. 42, Last annotation update) DB Crinia-angiotensin II OS Crinia georgiana (Quacking frog). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachinae; Crinia. RN 8374; SEQUENCE							
Query Match: BELONGS TO THE SERPIN FAMILY.							
DR	A60624; A60624;	PIR; A90917; A90917;	DR	ANGT-TRIGE	STANDARD;	PRT;	11 AA.
DR	InterPro; IPR00215; Serpin.	DR	ANGT CRIGE	STANDARD;	PRT;	11 AA.	
DR	PROSITE; PS0284; SERPIN; PARTIAL.	AC	209057;				
VASSOCONSTRICCTOR; PLASMA; Serpin.	PT	ANGT-TRIGE	STANDARD;				
KW	ANGIOTENSIN I.	PT	ANGT CRIGE	STANDARD;			
ANGIOTENSIN II.	PEPTIDE	ANGIOTENSIN III.	PT	ANGT-TRIGE	STANDARD;		
ANGIOTENSIN III.	PEPTIDE	ANGIOTENSIN III.	PEPTIDE	ANGT CRIGE	STANDARD;		
ANGIOTENSIN III.	FT	ANGIOTENSIN III.	FT	ANGT-TRIGE	STANDARD;		
ANGIOTENSIN III.	NON-TER	ANGIOTENSIN III.	NON-TER	ANGT CRIGE	STANDARD;		
SEQUENCE	8 AA;	1046 MW;	SEQUENCE	8 AA;	1046 MW;	SEQUENCE	8 AA;
Query Match: BELONGS TO THE SERPIN FAMILY.	Score: 36;	DB 1;	Query Match: BELONGS TO THE SERPIN FAMILY.	Score: 36;	DB 1;	Query Match: BELONGS TO THE SERPIN FAMILY.	Score: 36;
Best Local Similarity: 85.7%;	Pred. No. 1.3e+0		Best Local Similarity: 85.7%;	Pred. No. 1.3e+0		Best Local Similarity: 85.7%;	Pred. No. 1.3e+0
Matches 6; Conservative 0; Mismatches 0;			Matches 6; Conservative 0; Mismatches 0;			Matches 6; Conservative 0; Mismatches 0;	
2y	1 RYVYAHFF 7		2y	1 RYVYAHFF 7			
Dy	2 RYVYAHFF 8		Dy	2 RYVYAHFF 8			

RESULT 7
 ANG₁ SHEEP STANDARD; PRT; 476 AA.
 ID ANG₁ SHEEP
 AC P20757;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen precursor [Contains: Angiotensin I (Ang I);
 DE Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp₁);
 DE Angiotensin II (Ang II)].
 AGT OR SERPINAS.
 OS Ovis aries (Sheep).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Fecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID:9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=95072318; PubMed=7765514;
 RA Nagase M.; Suzuki F.; Furukawa A.; Takeda N.; Takeuchi K.;
 RA Murakami K.; Nakamura Y.;
 RT "Sequencing and expression of sheep angiotensinogen cDNA.";
 RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
 RN [2]
 RP SEQUENCE OF 25-39.
 RX MEDLINE=96136099; PubMed=3081342;
 RA Fernley R.T.; John M.; Niall H.D.; Coghlan J.P.;
 RT "Purification and characterization of ovine angiotensinogen.";
 RL Eur. J. Biochem. 154:597-601(1986).
 DE :!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 DE CLEAVES ANGiotensin I, FROM ANGiotensinogen. ACE (ANGiotensin
 DE CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGiotensin II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC :!- SUBCELLULAR LOCATION: Secreted.
 CC :!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC Plasma.
 CC :!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

RESULT 6
 ANG₁ HORSE STANDARD; PRT; 14 AA.
 ID ANG₁ HORSE
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Angiotensinogen (Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp₁-angiotensin II)).
 DE (Fragment).
 GN AGT OR SERPINAS.
 OS Equus caballus (Horse).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID:9736;
 RN [1]
 RP SEQUENCE.
 RA Skegg L.T. Jr., Kahn J.R., Lertz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate.",
 RL J. Exp. Med. 106:439-453(1957).
 DE :!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGiotensin I, FROM ANGiotensinogen. ACE (ANGiotensin
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGiotensin II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC :!- SUBCELLULAR LOCATION: Secreted.
 CC :!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC Plasma.
 CC :!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

RESULT 5
 ANG₁ PIR STANDARD; PRT; 11 AA.
 ID ANG₁ PIR
 AC P000215;
 DT 15-OCT-91.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00384; SERPIN; PARTIAL.
 KW Vasconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGiotensin I.
 FT PEPTIDE 1 8 ANGiotensin II.
 FT PEPTIDE 2 8 ANGiotensin III.
 FT NON-TER 14 14
 SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8E8EFBD7 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 14;
 Best Local Similarity 85.7%; Pred. No. 0.23; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;
 Qy 1 RYVAHPP 7
 Db 2 RYV1HPP 8

RESULT 4
 ANG₁ SHEEP STANDARD; PRT; 476 AA.
 ID ANG₁ SHEEP
 AC P20757;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensinogen precursor [Contains: Angiotensin I (Ang I);
 DE Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp₁);
 DE Angiotensin II (Ang II)].
 AGT OR SERPINAS.
 OS Ovis aries (Sheep).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Fecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID:9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=95072318; PubMed=7765514;
 RA Nagase M.; Suzuki F.; Furukawa A.; Takeda N.; Takeuchi K.;
 RA Murakami K.; Nakamura Y.;
 RT "Sequencing and expression of sheep angiotensinogen cDNA.";
 RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
 RN [2]
 RP SEQUENCE OF 25-39.
 RX MEDLINE=96136099; PubMed=3081342;
 RA Fernley R.T.; John M.; Niall H.D.; Coghlan J.P.;
 RT "Purification and characterization of ovine angiotensinogen.";
 RL Eur. J. Biochem. 154:597-601(1986).
 DE :!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 DE CLEAVES ANGiotensin I, FROM ANGiotensinogen. ACE (ANGiotensin
 DE CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGiotensin II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC :!- SUBCELLULAR LOCATION: Secreted.
 CC :!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC Plasma.
 CC :!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

RESULT 3
 ANG₁ PIR STANDARD; PRT; 11 AA.
 ID ANG₁ PIR
 AC P000215;
 DT 15-OCT-91.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00384; SERPIN; PARTIAL.
 KW Vasconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGiotensin I.
 FT PEPTIDE 1 8 ANGiotensin II.
 FT PEPTIDE 2 8 ANGiotensin III.
 FT NON-TER 14 14
 SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8E8EFBD7 CRC64;
 Query Match 87.8%; Score 36; DB 1; Length 476;
 Best Local Similarity 85.7%; Pred. No. 7.3; Mismatches 1; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Indels 0; Gaps 0;
 Qy 1 RYVAHPP 7
 Db 2 RYV1HPP 32

Matches	6;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;		
Qy	1	RVYAPPF	7							Circ. Res. 60:786-790(1987).	
Do	26	RVYIHPF	32							[6] SEQUENCE OF 34-45, AND SUBUNITS.	
RESULT 1.0											
ANG_HUMAN	STANDARD	PRT	485 AA.							RP	
AC	P01019; Q16359; Q96F91;									RC	SEQUENCE OF 34-45, AND SUBUNITS.
DT	21-JUL-1986 (Rel. 01, Created)									RC	TISSUE=SERUM;
DT	21-JUL-1986 (Rel. 01, Last sequence update)									RC	MEDLINE=95193954; PubMed=7533791;
DT	15-SEP-2003 (Rel. 42, Last annotation update)									RA	Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin Z., Stigbrand T., Gleich G.J., Sottrup-Jensen L., "Identification of angiotensinogen and complement C3dg as novel proteins binding the proform of eosinophil major basic protein in human pregnancy serum and plasma.", J. Biol. Chem. 270:13645-13651(1995).
DE	Angiotensinogen precursor [contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp [1]-angiotensin II)].									RA	SEQUENCE OF 34-43.
DE	Angiotensinogen precursor [contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp [1]-angiotensin II)].									RA	"Enzymatic degradation and electrophoresis of human angiotensin I.", Biochim. Biophys. Acta 168:106-112(1966).
GN	AGT OR SERPINAS.									RA	[7] RT
OS	Homo sapiens (Human).									RA	Proteins binding the proform of eosinophil major basic protein in human pregnancy serum and plasma.", J. Biol. Chem. 270:13645-13651(1995).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									RA	SEQUENCE OF 34-43.
OX										RA	"Enzymatic degradation and electrophoresis of human angiotensin I.", Biochim. Biophys. Acta 168:106-112(1966).
RN										RA	[8] RT
RP	SEQUENCE FROM N.A. NCBITaxonID=9616;									RA	Carbohydrate-Linkage Sites
RX	MEDLINE=B9170129; PubMed=2924688;									RA	MEDLINE=86056581; PubMed=3934016;
RA	Gaillard I., Clauser E., Corvol P.; "Structure of human angiotensinogen gene.", DNA 8:87-99 (1989).									RA	Campbell D.J., Boulni J., Coezy B., Menard J., Corvol P.; "Processing of rat and human angiotensinogen precursors by microsomal membranes.", Mol. Cell. Endocrinol. 43:31-40(1985).
RN										RA	[9] RT
RP	SEQUENCE FROM N.A. NCBITaxonID=9616;									RA	FUNCTION OF ANGIOTENSIN III.
RX	MEDLINE=B9170129; PubMed=2924688;									RA	MEDLINE=75166949; PubMed=9130282;
RA	Goodfriend T.L., Peach M.J.; "Angiotensin III: (D-Des-Aspartic Acid-1)-Angiotensin III. Evidence and speculation for its role as an important agonist in the renin-angiotensin system.", Circ. Res. 36:38-48(1975).									RA	Goodfriend T.L., Peach M.J.; "Angiotensin III: (D-Des-Aspartic Acid-1)-Angiotensin III. Evidence and speculation for its role as an important agonist in the renin-angiotensin system.", Circ. Res. 36:38-48(1975).
RN										RA	[10] RT
RP	STRUCTURE BY NMR OF ANGIOTENSIN III.									RA	STRUCTURE BY NMR OF ANGIOTENSIN III.
RX	MEDLINE=98151281; PubMed=9493317;									RA	MEDLINE=98151281; PubMed=9493317;
RA	Carpenter K.A., Wilkes B.C., Schiiller P.W.; "The octapeptide angiotensin III adopts a well-defined structure in a phospholipid environment.", J. Biol. Chem. 251:448-453(1998).									RA	[11] RT
RX	MEDLINE=92008239; PubMed=139429;									RA	VARIANTS MET-207; THR-268 AND CYS-281.
RA	Jeunemaitre X., Sobrier F., Kotelevtsev Y.V., Lifton R.P.; "The octapeptide angiotensin III adopts a well-defined structure in a phospholipid environment.", J. Biol. Chem. 251:448-453(1998).									RA	MEDLINE=92008239; PubMed=139429;
RX	MEDLINE=93291876; PubMed=8513325;									RA	VARIANTS MET-207; THR-268 AND CYS-281.
RA	VARIANT THR-268.									RA	MEDLINE=93291876; PubMed=8513325;
RX	MEDLINE=921291876; PubMed=8622667;									RA	VARIANT THR-268.
RA	Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T., Celerier J., Pau B., Corvol P., Jeunemaitre X.; "The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).									RA	MEDLINE=921291876; PubMed=8622667;
RX	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).									RA	Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T., Celerier J., Pau B., Corvol P., Jeunemaitre X.; "The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).
RA										RA	[12] RT
RX	VARIANTS ILE-242; ARG-244 AND CYS-281.									RA	VARIANTS ILE-242; ARG-244 AND CYS-281.
RA	Hixson J.E., Powers P.K.; "Detection and characterization of new mutations in the human angiotensinogen gene (AGN).", RT									RA	MEDLINE=95231754; PubMed=7607642;
RX	"A molecular variant of angiotensinogen associated with preclampsia.", Hum. Genet. 96:110-112(1993).									RA	Hixson J.E., Powers P.K.; "Detection and characterization of new mutations in the human angiotensinogen gene (AGN).", RT
RA										RA	"A molecular variant of angiotensinogen associated with preclampsia.", Hum. Genet. 96:110-112(1993).
RX	VARIANTS ILE-242; ARG-244 AND CYS-281.									RA	[13] RT
RA	Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T., Celerier J., Pau B., Corvol P., Jeunemaitre X.; "The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).									RA	MEDLINE=95231754; PubMed=7607642;
RX	"The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).									RA	Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T., Celerier J., Pau B., Corvol P., Jeunemaitre X.; "The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).
RA										RA	[14] RT
RX	CHARACTERIZATION OF VARIANT CYS-281.									RA	CHARACTERIZATION OF VARIANT CYS-281.
RA										RA	MEDLINE=95199253; PubMed=8622667;
RX	Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T., Celerier J., Pau B., Corvol P., Jeunemaitre X.; "The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).									RA	Gimenez-Roqueplo A.P., Leconte I., Cohen P., Simon D., Guyene T.T., Celerier J., Pau B., Corvol P., Jeunemaitre X.; "The natural mutation Y248C of human angiotensinogen leads to abnormal glycosylation and altered immunological recognition of the protein.", J. Biol. Chem. 271:9838-9844(1996).
RA										RA	[15] RT
RX	SEQUENCE OF 1-338 FROM N.A.									RA	SEQUENCE OF 1-338 FROM N.A.
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).									RA	MEDLINE=95231754; PubMed=7607642;
RX	SEQUENCE OF 1-338 FROM N.A.									RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA										RA	[16] RT
RX	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).									RA	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA										RA	[17] RT
RX	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).									RA	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA										RA	[18] CC
RX	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).									RA	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA										RA	[19] CC
RX	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).									RA	"Molecular cloning of human angiotensinogen cDNA and evidence for the presence of its mRNA in rat heart.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.

-!- FUNCTION: Angiotensin III stimulates aldosterone-linked 2.2 heterotramer with the proform of PRG2 and as a complex (probably a 2:2:2 heterohexamer) with pro-PRG2 and C3d5g.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the plasma.

-!- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION (PIH) (PREECLAMPSIA).

-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

-!- CAUTION: IT IS UNCERTAIN WHETHER MET-10 IS THE INITIATOR.

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EMBL: K02215; AAAI1731; 1; -.

EMBL: M24689; ARAA1679; 1; -.

EMBL: M24686; AAAA1679; 1; JOINED.

EMBL: M24687; AAAA1679; 1; JOINED.

EMBL: M24688; AAAA1679; 1; JOINED.

EMBL: M24689; AAAA1679; 1; JOINED.

EMBL: X15324; CAA33385; 1; -.

EMBL: X15325; CAA33385; 1; JOINED.

EMBL: X15326; CAA33385; 1; JOINED.

EMBL: X15327; CAA33385; 1; JOINED.

EMBL: M69110; AAA2282; 1; -.

EMBL: BC011519; AAH11519; 1; -.

EMBL: S78529; AAD14287; 1; -.

EMBL: S78530; AAD14288; 1; -.

PIR: A35203; ANHU.

SWISS-2DPAGE: P01G19; HUMAN.

Gene: HGNC:333; AGT.

MM: 106150; -.

DR: GO:000565; C:Soluble fraction; TAS.

GO: GO:000486; F:serine protease inhibitor activity; TAS.

PRINTS: PRO00654; serpin; 1.

DR: GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.

DR: GO:0007267; P:cell-cell signaling; TAS.

GO: GO:0017565; P:pregnancy; TAS.

GO: GO:0008217; P:regulation of blood pressure; TAS.

InterPro: IPR000027; Angiotensin.

InterPro: IPR000215; Serpin.

DR: GO:000565; C:Soluble fraction; TAS.

PRINTS: PRO00654; ANGIOTENSIN I.

SMART: SM00093; SERPIN; 1.

PROSITE: PS00284; SERPIN; 1.

KW: vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;

Disease mutation; Polymorphism.

SIGNAL 1 33 Score 36; DB 1; Length 485;

CHAIN 34 485 ANGIOTENSIN

PEPTIDE 34 43 ANGIOTENSIN I.

PEPTIDE 34 41 ANGIOTENSIN II.

PEPTIDE 35 41 ANGIOTENSIN III.

CARBOHYD 47 47 N-LINKED (GLCNAC. . .).

CARBOHYD 170 170 N-LINKED (GLCNAC. . .).

Best Local Similarity 87.8%; Score 36; DB 1; Length 485;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 1;

1 PREGNANCY

RESUME 12

H15	DROME	STANDARD;	PRT;	544 AA.
AC	H15_DROME			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 41, Last annotation update)			
DE	T-box protein H15.			
GN	H15.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OB	Bivalvia; Drosophilidae; Drosophila.			
OX	NCBI_TAXID:7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Brook W.J.; Cohen S.M.;			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
CC	-- SUBCELLULAR LOCATION: Nuclear (Potential).			
CC	-- SIMILARITY: Contains 1 T-box domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	SEQUENCE FROM N.A.			
DR	X98766; CAA67304.1; -.			
DR	HSSP; P04781; IXB.R.			
DR	InterPro; IPR001699; TF_T-box.			
DR	Protein; PF00907; T-box; 1.			
DR	PRINTS; PRO0937; TBOX.			
DR	SMART; SM00425; TBOX.			
DR	PROSITE; PS01283; TBOX_1.			
DR	PROSITE; PS01264; TBOX_2; FALSE NEG.			
DR	PROSITE; PS50232; TBOX_3; 1.			
KW	DNA-binding; Nuclear protein.			
FT	DOMAIN 56 59			
FT	DOMAIN 83 91			
FT	DOMAIN 118 125			
FT	DOMAIN 170 356			
FT	DOMAIN 242 245			
FT	DOMAIN 436 443			
SEQUENCE	544 AA; 600:0 MW; 4D4DBB8E78244132 CRC64;			
Qy	1 RYIAHP 6			
Db	247 RYIAHP 252			
RESULT 13				
GLYA_METTM	STANDARD;	PRT;	424 AA.	
AC	GLYA_METTM			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase).			
DE	GLYA.			
GN	Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).			
OS	Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;			
OC	Methanobacteriaceae; Methanobacteria; Methanothermobacter.			
OC	NCBI_TAXID=79929;			
OX	NCBI_TAXID=79929;			

RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9184910; PubMed=8617278;			
RA	Vaupel M., Diez H., Linder D., Thauer R.K.;			
RA	"Primary structure of cyclohydrolase (Mch) from Methanobacterium thermoautotrophicum (strain Marburg) and functional expression of the mch gene in Escherichia coli."			
RT	Eur. J. Biochem. 216:294-300 (1996).			
CC	-- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.			
CC	-- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine + (H ₂ O) = tetrahydrofolate + L-serine.			
CC	-- COFACTOR: Pyridoxal phosphate (By similarity).			
CC	-- PATHWAY: Key enzyme of purines, lipids, hormones and other components.			
CC	-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-- SIMILARITY: BELONGS TO THE SHMT FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	SEQUENCE FROM N.A.			
CC	DR HSSP; P0477; IDFO.			
CC	DR HAMAP; MF_00051; 1.			
CC	DR InterPro; IPR01085; Gly_HyMetransf.			
CC	DR Pfam; PF00464; SHMT; 1.			
CC	DR PROSITE; PS00036; SHMT; 1.			
CC	DR KWN: Pyridoxal phosphate; One-carbon metabolism.			
CC	DR FT BINDING 227			
CC	DR SQ SEQUENCE 424 AA; 47076 MW; BPF867AA115871956 CRC64;			
CC	Qy Query Match 80.5%; Score 33; DB 1; Length 424;			
CC	CC Best Local Similarity 57.1%; Pred. No. 26; Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;			
CC	Qy - RYIAHP 7			
CC	Db 237 KIYTHPF 143			
RESULT 14				
GLGC_HAEIN	STANDARD;	PRT;	437 AA.	
ID	GLGC_HAEIN			
AC	P43766;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DE	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucoside pyrophosphorylase) (ADPGIC Pase).			
GN	GLGC OR H11359.			
OS	Haemophilus influenzae			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
R2	SEQUENCE FROM N.A.			
RC	STRAIN-RD / KW20 / ATCC 51907;			
RX	MEDLINE=95350610; PubMed=7543800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Blattner F.R., Liou L.-I., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.P., Phillips C.A., Spriggs T., Redblom E., Cottrell M.D., Utterback T.R., Hama M.C., Nguyen D.T., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;			
RA	"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd." ,			
RA	Science 269:496-512 (1995).			

-!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =

CC diiphosphate + ADP glucose.

CC -!- PATHWAY: Glycogen biosynthesis; first step.

CC -!- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-

CC PHOSPHATE ADENYLYLTRANSFERASE FAMILY.

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CC EMBL: U31515; AAC23006.1; ALT_INIT.

DR PIR: B64119; B64119.

DR TIGR: H11359; -.

DR HAMAP: MF_00624; -; -.

DR InterPro: IPR005836; NTP_Glu_PyroP.

DR InterPro: IPR005835; NTP_Transferase.

DR PFam: PF00483; NTP_Transferase; -.

DR PROSITE: PS000808; ADP_Glc_Pyrophosphoryltransferase_1;

DR PROSITE: PS000809; ADP_Glc_Pyrophosphoryltransferase_2;

DR PROSITE: PS000810; ADP_Glc_Pyrophosphoryltransferase_3;

KW Glycogen biosynthesis; Transferase; Nucleotidyltransferase;

KW Complete proteome.

SEQUENCE 437 AA; 49105 MW; ESE2284ACESAD19 CRC44;

Query Match 80.5%; Score 33; DB 1; Length 439;

Best Local Similarity 83.3%; Pred. No. 27;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VYAHFF 7

Dd 254 LYAHFF 259

RESULT 15

GLGC_PASMU
ID GLGC_PASMU
AC 09CN9.;
DT 15-SEP-2003 (Rel: 42; Created)
DT 15-SEP-2003 (Rel: 42; Last sequence update)

DT 15-SEP-2003 (Rel: 42; Last annotation update)
DE Glucosidase-1-phosphate adenyllyltransferase (EC 2.7.7.27) (ADP-glucose
DE synthase) (ADP-glucose Pyrophorylase) (ADPGlc Pase).

GN GLGC OR PM0543.

OS Pasteurella multocida.

CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

CC Pasteurellaceae; Pasteurella.

CC NCBI TaxID:747;

CC RN [1]

CC RP SEQUENCE FROM N.A.

CC RC MEDLINE=21145866; PubMed=11248100;

CC RX May B.J., Zhang Q., Li L.L., Paustian M.L., Whiteman T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:3463-3465 (2001).

CC -!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =

CC diiphosphate + ADP glucose.

CC -!- PATHWAY: Glycogen biosynthesis; first step.

CC -!- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-

CC PHOSPHATE ADENYLYLTRANSFERASE FAMILY.

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CC EMBL: AE0006089; AAK02627.1; -.

DR

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OM protein - protein search, using sw model

Run on:

November 5, 2003, 18:10:26 / Search time 53 Seconds
(without alignments)
34.082 Million cell updates/sec

Title: US-09-772-819-18

Perfect score: 41

Sequence: 1 RYVAAHFF 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_moth:*

8: sp_oragne:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteria:*

17: sp_archaea:*

17 34 82.9 5 Q8IMU0
18 34 82.9 5 Q9PB20
19 34 82.9 5 Q9VR3
20 33 80.5 2 Q8KNT2
21 33 80.5 185 17 Q8JLA7
22 33 80.5 225 2 Q93I46
23 33 80.5 439 16 Q9CN92
24 33 80.5 728 5 Q9VFT7
25 33 80.5 751 5 060975
26 33 80.5 842 5 Q815V4
27 33 80.5 997 10 Q9AHV1
28 33 80.5 1074 10 Q8SS88
29 33 80.5 1144 2 Q9AN19
30 32 78.0 176 16 Q8ZRW3
31 32 78.0 176 16 Q8Z9K1
32 32 78.0 176 16 Q8XA24
33 32 78.0 177 2 Q9X75
34 32 78.0 211 16 Q06366
35 32 78.0 212 17 Q8ZBM9
36 32 78.0 299 11 Q8BX64
37 32 78.0 331 12 Q71094
38 32 78.0 336 17 Q8RTT5
39 32 78.0 358 10 Q82239
40 32 78.0 395 8 Q9TH87
41 32 78.0 401 2 Q30774
42 32 78.0 424 16 P95084
43 32 78.0 431 16 Q82233
44 32 78.0 482 10 Q39499
45 32 78.0 508 5 Q9BLR4

ALIGNMENTS

RESULT 1
ID Q9PS07 PRELIMINARY:
AC Q9PS07:
DT 01-MAY-2000 (TREMBREL 13; Created)
DT 01-MAY-2000 (TREMBREL 13; Last sequence update)
DT 01-MAY-2000 (TREMBREL 13; Last annotation update)
RA Stephens G.A., Sakakibara S.,
RT "New angiotensin I isolated from a reptile, Alligator mississippiensis."
OS Alligator mississippiensis (American alligator),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Alligatoridae; Alligator; Alligator.
NCBI_TaxID=8496;
OX [1]
RN [1]
RP SEQUENCE.
RX YEDLINE=93307610; PubMed=8319878;
RA Takei Y., Sillendorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA Stephens G.A., Sakakibara S.,
RT Gen. Comp. Endocrinol. 90:214-219 (1993).
RL SEQUENCE 10 AA; 12:6 MW;
SQ CEE38DD761F2DB42 CRC64;

Query Match Score 90.2%; Score 37; DB 13; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.54%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
ID Q8JH29 PRELIMINARY:
AC Q8JH29:
DT 01-OCT-2002 (TREMBREL 22; Created)
DT 01-OCT-2002 (TREMBREL 22; Last sequence update)
DT 01-MAR-2003 (TREMBREL 23; Last annotation update)
DE Angiotensinogen precursor.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	37	90.2	10	13	Q9PS07	Q9PS07 alligator m	
2	37	90.2	454	13	Q8JH29	Q8JH29 brachydarilo	
3	36	87.8	14	5	Q10757	Q10757 cheronyzon	
4	36	87.8	222	11	Q8BX6	Q8BX6 mus musculus	
5	36	87.8	244	11	C8DZ2	Q8DZ2 mus musculus	
6	36	87.8	245	6	Q95J13	Q95J13 pan troglody	
7	36	87.8	477	4	Q9FJ5	Q9FJ5 homo sapiens	
8	36	87.8	477	11	Q8VCN0	Q8VCN0 mus musculus	
9	36	87.8	485	6	Q9GLN8	Q9GLN8 pan troglody	
10	36	87.8	485	6	Q9GLP7	Q9GLP7 pan troglody	
11	36	87.8	485	6	Q9GLP6	Q9GLP6 gorilla gorilla	
12	36	87.8	486	6	Q9TS20	Q9TS20 callithrix	
13	36	87.8	716	11	Q9J07	Q9J07 mus musculus	
14	36	87.8	719	11	Q9DBQ0	Q9DBQ0 mus musculus	
15	35	85.4	146	16	Q8ZLA3	Q8ZLA3 salmonella	
16	35	85.4	146	16	Q8Z2A6	Q8Z2A6 salmonella	

OS Brachydanio rerio (Zebrafish); (*Danio rerio*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Ostariophysi; Cypriniformes;
 OC Cyprinidae; *Danio*.
 OX NCBI_TaxID:7355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen M., Vallon V., Schnermann J.B., Endo Y., Smart J., Smart A.,
 RA Briggs J.P.;
 RA "Cathepsin D is responsible for angiotensin generation in zebrafish.";
 RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL !- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC EX973; AAL2168.1; -.
 DR InterPro: IPR000227; Angiotensin.
 DR InterPro: IPR000215; Serpin.
 DR PF0079; serpin; 1.
 DR PRINTS; PRO0054; ANGOTNSNGN.
 DR SM0093; SERPIN.
 DR PROSITE; PS00284; SERPIN; 1.
 DR PROSTE; PSC00284; SERPIN; 1.
 KW Procase inhibitor; Serine protease inhibitor; Serpin; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 28 ANGOTENSIN 1.
 SQ SEQUENCE 454 AA; 51058 MW; 688A1D4EB2E14E38 CRC64;
 Query Match Score 37; DB 13; Length 454;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RVYAHPP 7
 Db 20 RVYVHPF 26

RESULT 3
 Q10757 PRELIMINARY; PRT; 14 AA.
 ID Q10757
 AC Q10757; PRELIMINARY; PRT; 14 AA.
 DT 01-NOV-1996 (TREMBLrel. 01; Created)
 DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08; Last annotation update)
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdilia; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID:13286;
 RN [1]
 RP SEQUENCE; PubMed=7637887;
 RX Laurent V., Bulet P., Salzet M.A.;
 RA "Comparison of the leech *Theromyzon tessulatum* angiotensin I-like molecule with forms of vertebrate angiotensinogens: a hormonal system conserved in the course of evolution.";
 RT RN
 SEQUENCE=BRAIN;
 RC MEDLINE=96201949; PubMed=8612806;
 RX Laurent V., Salzet M.;
 RA "Metabolism of angiotensins by head membranes of the leech *Theromyzon tessulatum*."
 RT FEBS Lett. 384:123-127 (1996).
 CC !- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.
 KW Glycoprotein; Serpin.
 PT NON
 SQ SEQUENCE 14 AA; 1763 MW; 335169D88EEFBDD7 CRC64;
 Query Match Score 36; DB 5; Length 14;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RVYAHPP 7
 Db 2 RVYVHPF 8

RESULT 4
 Q8BZ6 PRELIMINARY; PRT; 222 AA.
 ID Q8BZ6
 AC Q8BZ6; PRELIMINARY; PRT; 222 AA.
 DT 01-MAR-2003 (TREMBLrel. 23; Created)
 DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)
 DE SEC14-like protein 1 homolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 MEDLINE=22334683; PubMed=12466851;
 RX The RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of the RIKEN Genome Exploration Research Group Phase I & II Team; RT 60,770 full-length cDNAs.";
 RT Nature 420:553-557 (2002).
 RL EMBL; AK047396; BAC33044.1; -.
 DR SEQUENCE 222 AA; 25370 MW; BFBCE22530BEC4A CRC64;
 SQ Query Match Score 87.8%; DB 11; Length 222;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RVYAHPP 7
 Db 10 RVYHPP 16

RESULT 5
 Q8CD22 PRELIMINARY; PRT; 244 AA.
 ID Q8CD22
 AC Q8CD22; PRELIMINARY; PRT; 244 AA.
 DT 01-MAR-2003 (TREMBLrel. 23; Created)
 DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 MEDLINE=22334683; PubMed=12466851;
 RX The RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of the RIKEN Genome Exploration Research Group Phase I & II Team; RT 60,770 full-length cDNAs.";
 RT Nature 420:553-557 (2002).
 RL EMBL; AK029331; BAC2639.1; -.
 DR HYPOTHETICAL PROTEIN.
 SQ Query Match Score 87.8%; DB 11; Length 244;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 RVYAHPP 7
 Db 173 RVYHPP 178

RESULT 6
 Q95J13 PRELIMINARY; PRT; 245 AA.
 ID Q95J13
 AC Q95J13;

01-DEC-2001 (TREMBLrel. 19, Created)
 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 Angiotensinogen (Fragment).
 REN.
 Pan Troglodytes (Chimpanzee); Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 NCBI_TaxID=9598;
 [1]
 SEQUENCE FROM N.A.
 RP STRAIN:504, and 505;
 Satta Y.;
 "Comparison of DNA and protein polymorphisms between humans and
 chimpanzees";
 Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 EMBL: AB062027; BAB55856; 1;
 EMBL; AB062028; BAB55857; 1;
 InterPro; IPR000227; Angiotensinogen.
 InterPro; IPR000215; Serpin.
 Pfam; PF00079; serpin; 1
 PRINTS; PRO0654; ANGIOESENSGN.
 Protease inhibitor; Serine protease inhibitor; Serpin.
 NON_TER 245; 245;
 SEQUENCE 245 AA; 26317 NR; E009239039803E0B CRC64;
 Query Match 87.8%; Score 36; DB 6; Length 245;
 Best Local Similarity 85.7%;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

1 RYVYAHPPF 7
 |||||
 35 RYVYIHPPF 4 1

RESULT 7
 ID Q96FD5 PRELIMINARY;
 Q96FD5; 19, Created)
 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 01-MAR-2003 (TREMBLrel. 19, Last annotation update)
 Similar to angiotensinogen.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 RP TISSUE=brain;
 Satta Y.;
 "Comparison of DNA and protein polymorphisms between humans and
 chimpanzees";
 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 EMBL: BCO1231; AAH11231; 1;
 InterPro; IPR000227; Angiotensinogen.
 InterPro; IPR000215; Serpin.
 Pfam; PF00079; serpin; 1
 PRINTS; PRO0654; ANGIOESENSGN.
 Protease inhibitor; Serine protease inhibitor; Serpin.
 SEQUENCE 477 AA; 51985 MW; AB79BB70532FDE2
 CRC64;
 Query Match 87.8%; Score 36; DB 11; Length 477;
 Best Local Similarity 85.7%;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

1 RYVYAHPPF 7
 |||||
 26 RYVYIHPPF 32

RESULT 9
 ID Q96JNB PRELIMINARY;
 Q96JNB; 16, Created)
 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 Human-Chimpanzee DNA sequence variation in the four major genes of
 the renin angiotensin system.";
 Genomics 69:14-26 (2000).
 RT
 Pan troglodytes (Chimpanzee).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 NCB_TaxID=9598;
 [1]
 SEQUENCE FROM N.A.
 RP TISSUE=brain;
 Satta Y.;
 "Comparison of DNA and protein polymorphisms between humans and
 chimpanzees";
 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 EMBL: BCO1231; AAH11231; 1;
 InterPro; IPR000227; Angiotensinogen.
 InterPro; IPR000215; Serpin.
 Pfam; PF00079; serpin; 1
 PRINTS; PRO0654; ANGIOESENSGN.
 Protease inhibitor; Serine protease inhibitor; Serpin.
 SEQUENCE 517 AA; 51985 MW; AB79BB70532FDE2
 CRC64;
 Query Match 87.8%; Score 36; DB 4; Length 477;
 Best Local Similarity 85.7%;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

1 RYVYAHPPF 7
 |||||
 26 RYVYIHPPF 32

RESULT 8
 ID Q8VCN0 PRELIMINARY;
 Q8VCN0; 20, Created)
 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 01-MAR-2002 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Angiotensinogen).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 Straussberg R.;
 Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RA
 RL
 RN
 SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 Straussberg R.;
 Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RA
 CC !- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR BC019496; AAH19496; 1;
 EMBL; BC028877; AAH28877; 1;
 DR InterPro; IPR000227; Angiotensinogen.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1
 DR PRINTS; PRO0654; ANGIOESENSGN.
 DR Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
 KW Serpin.
 SEQUENCE 477 AA; 51985 MW; AB79BB70532FDE2
 CRC64;
 Query Match 87.8%; Score 36; DB 11; Length 477;
 Best Local Similarity 85.7%;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

1 RYVYAHPPF 7
 |||||
 26 RYVYIHPPF 32

RESULT 9
 ID Q96JNB PRELIMINARY;
 Q96JNB; 16, Created)
 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 Human-Chimpanzee DNA sequence variation in the four major genes of
 the renin angiotensin system.";
 Genomics 69:14-26 (2000).
 RT
 Pan troglodytes (Chimpanzee).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 NCB_TaxID=9598;
 [1]
 SEQUENCE FROM N.A.
 RP TISSUE=brain;
 Dufour C., Casane D., Denton D., Corvol P.,
 Jeunemaitre X.;
 "Human-Chimpanzee DNA sequence variation in the four major genes of
 the renin angiotensin system.";
 Genomics 69:14-26 (2000).
 RT
 EMBL; AF193458; AAG30306; 1;
 DR
 EMBL; AF193459; AAG30306; 1;
 DR
 EMBL; AF193460; AAG30306; 1;
 DR InterPro; IPR000227; Angiotensinogen.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1
 DR PRINTS; PRO0654; ANGIOESENSGN.
 DR SMART; SM00093; SERPIN; 1
 DR PROSITE; PS0284; SERPIN; 1
 DR PROSITE inhibitor; Serine protease inhibitor; Serpin.
 KW

SQ	SEQUENCE	485 AA;	53110 MW;	C14C67E49A53F05F CRC64;	DR	Pfam; PF00079; serpin; 1.
	Query Match	87.8%;	Score 36;	DB 6;	DR	PRINTS; PR00654; ANGIOTENSNGN.
	Best Local Similarity	85.7%;	Pred. No. 44;		DR	SMART; SM00093; SERPIN; 1.
Matches	6; Conservative	0;	Mismatches	1;	DR	PROSITE; PS0028A; SERPIN; 1.
					KW	Protease inhibitor; Serine Protease inhibitor; Serpin.
					SEQUENCE	485 AA;
Qy	1 RYVYAHPF 7				53186 MW;	53BC9235271C8255 CRC64;
Db	35 RYVYIHPF 41					
RESULT 10					Query Match	87.8%;
Q9GLP7	PRELIMINARY;				Best Local Similarity	85.7%;
ID	Q9GLP7				Matches	6;
AC		PRT;	485 AA.		Indels	0;
DT	01-MAR-2001	(TREMBLrel.	16;		Gaps	0;
DT	01-MAR-2001	(TREMBLrel.	16;			
DT	01-OCT-2002	(TREMBLrel.	22;	Last annotation update;		
DE						
Angiotensinogen.						
GN						
PAN						
Pan troglodytes (Chimpanzee).						
OC						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC						
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.						
OX						
RN						
[1]						
SEQUENCE FROM N.A.						
SHATTUCK-EDENS D., MCGRAIL M., STONE S.;						
RT						
"Germline mutations in the angiotensinogen gene cause predisposition						
RT						
to type 1 diabetes mellitus".						
RT						
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.						
CC						
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.						
DR						
EMBL: AAF18487; AAG29056 i.						
DR						
INTERPRO: IPR000227; Angiotensinogen.						
DR						
INTERPRO: IPR000215; Serpin.						
DR						
PRINTS; PR00654; ANGIOTENSNGN.						
DR						
SMART; SM00093; SERPIN; 1.						
DR						
PROSITE; PS0028A; SERPIN; 1.						
DR						
PROTEASE INHIBITOR; SERPIN; Serine protease inhibitor; Serpin.						
KW						
SEQUENCE 485 AA;						
Q9GLP6	PRELIMINARY;					
ID	Q9GLP6	PRT;	485 AA.			
AC						
DT	01-MAR-2001	(TREMBLrel.	16;	Created)	DR	Q99J07; PRELIMINARY;
DT	01-MAR-2001	(TREMBLrel.	16;	Last sequence update)	AC	Q99J07; PRELIMINARY;
DT	01-OCT-2002	(TREMBLrel.	22;	Last annotation update)	DT	01-JUN-2001 (TREMBLrel.
DE					17; Created)	
Angiotensinogen.					01-MAR-2003 (TREMBLrel.	
GN					23; Last annotation update)	
GORILLA gorilla (gorilla).					DE	RIKEN cDNA 1200017E04 gene.
OS					GN	1200017E04Rik.
OC					OS	Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC					OC	Mammalia; Eutheria; Primates; Catarrhini; Gorilla.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					NCBI_TaxID: 9593;	
OX					RN	[1]
RN					RP	SEQUENCE FROM N.A.
RA					RA	SHATTUCK-EDENS D., MCGRAIL M., STONE S.;
RT					RT	"Germline mutations in the angiotensinogen gene cause predisposition
RT					RT	to type 1 diabetes mellitus".
RL					RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
AGT.					CC	-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
GN					DR	AF188488; AAG29057; 1.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000227; Angiotensinogen.
OS					DR	InterPro; IPR000215; Serpin.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.					DR	InterPro; IPR000227; Angiotensinogen.
OX					DR	InterPro; IPR000215; Serpin.
RN					DR	InterPro; IPR000227; Angiotensinogen.
RN					DR	InterPro; IPR000215; Serpin.
RP					DR	InterPro; IPR000227; Angiotensinogen.
RA					DR	InterPro; IPR000215; Serpin.
RT					DR	InterPro; IPR000227; Angiotensinogen.
RT					DR	InterPro; IPR000215; Serpin.
RL					DR	InterPro; IPR000227; Angiotensinogen.
AGT.					DR	InterPro; IPR000215; Serpin.
GN					DR	InterPro; IPR000227; Angiotensinogen.
GORILLA gorilla (gorilla).					DR	InterPro; IPR000215; Serpin.
OS					DR	InterPro; IPR000227; Angiotensinogen.
OC					DR	InterPro; IPR000215; Serpin.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			</td			

RA RA RL RL Submitted (APR-2001) to the EXML/GerBank/DBJ databases.									
EMBL; B005766; AAH05766..1.									
MGD; MG-1..921386; 1200017EC4Rik.									
InterPro; IPR001251; CRAL_TRIO.									
InterPro; IPR0056797; MSF1_-.									
InterPro; IPR0056797; RetBnd/tocTrans.									
Pfam; PF00650; CRAL_TRIO_N; 1.									
Pfam; PF04707; MSF1_-.									
Pfam; PF0180; CREYINALDHPB.									
SMART; SM00516; SEC14; 1.									
DR PROSITE; PS50191; CRAL_TRIO; 1.									
DR PROSITE; PS50191; CRAL_TRIO; 1.									
DR SMART; SM00516; SEC14; 1.									
DR SEQUENCE; 716 AA; 81275 MW; 8CA55D06ABFEBB4 CRC64;									
DR SEQUENCE; 716 AA; 81275 MW; 8CA55D06ABFEBB4 CRC64;									
DR SEQUENCE; 716 AA; 81275 MW; 8CA55D06ABFEBB4 CRC64;									
Query Match	87.8%	Score 36:	DB 11;	Length 716;					
Best Local Similarity	85.7%	Pred. No.	65;						
Matches 6;	Conservative	0;	Mismatches	1;	Indels	C;	Caps	0;	
Qy:	1 RVIYAHPF 7								
Db:	10 RVIYKHPF 16								
RESULT 15									
Q9DBQ0	PRELIMINARY;	PRT;	719 AA.						
Q9DBQ0;	PRELIMINARY;	PRT;	719 AA.						
AC									
Q9DBQ0; 01-JUN-2001 (TREMBLre); 17; Created									
DT 01-JUN-2001 (TREMBLre); 1; Last annotation update)									
DT 01-MAR-2003 (TREMBLre); 23; Last annotation update)									
DE 1200017E04Rik									
GN 1200017E04Rik									
Mus musculus (Mouse)									
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.									
OC Mammalia; Matsuoka H.A.; Ashburrier M.; Batalov S.; Casavant T..; Fleischmann W.; Gaaster-and T.; Gissi C.; King B.; Kochiwa H.; Kuehl P.; Lewis S.; Matsuo Y.; Nikaido Y.; Pescce G.; Quackenbush J..; Schriml L.M.; Steubli F.; Suzuki R.; Tomita M.; Wagner L.; Washio T..; Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.; Blaize J.; Boffelli D.; BcJunga N.; Carninci P.; de Bonaldo M. F..; Brownseir M.J.; Bult C.; Fletcher C.; Fujita M.; Garijoaldi M..; Gustincich S.; Hill C.; Hofmann M.; Hume D.A.; Kamiya M.; Lee N.H..; Lyons P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombaerts P.; Nordone P.; Ring B.; Ringold M.; Rodriguez J.; Sakamoto N.; Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibusawa Y.; Storch K.-F..; Suwa H.; Toyo-oka K.; Wang K.H.; Weitz C.; Whittaker C.; Wilming L..; Wynshaw-Boris A.; Yoshida K.; Hasegawa Y.; Kawaji H.; Kohtsuki S..; Hayashizaki Y..;									
RA "Functional annotation of a full-length mouse cDNA collection."									
RA RLU									
DR EMBL; AK004918; BAB23589..1..									
DR Med; MG-1..921386; 1200017EC4Rik.									
DR InterPro; IPR001251; CRAL_TRIO.									
DR InterPro; IPR005697; MSF1_-.									
DR SMART; SM00516; SEC14; 1.									
DR PROSITE; PS50191; CRAL_TRIO; 1.									
DR SEQUENCE; 719 AA; 81750 MW; 6ACB31D4F5BAB7FF8 CRC64;									
Query Match	87.8%	Score 36:	DB 11;	Length 719;					